

GenCore version 5.1.6
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CM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:28:49 ; Search time 459.432 Seconds
(without alignments)
3138.794 Million cell updates/sec

Title: US-10-088-666-1

Perfect score: 267

Sequence: 1 tctatcggaagtaagaccct.....agtagtcgggagtcgccc 267

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Gapop 60.0, Gapext 60.0

Searched: 3625171 seqs, 2700493622 residues

Word size: 10

Total number of hits satisfying chosen parameters: 796812

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

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Published Applications_NA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	35	13.1	54	16	US-10-329-624-5036 Sequence 5036, App
6	35	13.1	187	8	US-08-781-986A-4682 Sequence 4682, App
7	35	13.1	187	16	US-10-329-624-4682 Sequence 4682, App
8	35	13.1	216	8	US-08-781-986A-4589 Sequence 4589, App
9	35	13.1	216	16	US-10-329-624-4589 Sequence 4589, App
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97 35 13.1 475 16 US-10-329-624-3621 Sequence 3621, Ap
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99 35 13.1 587 16 US-10-329-624-3554 Sequence 3554, Ap
100 35 13.1 596 8 US-08-781-986A-3596 Sequence 3596, Ap

ALIGNMENTS

RESULT 1
US-09-070-927A-359/c
; Sequence 359, Application US/09070927A
; Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Steven Barash
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 359:
SEQUENCE CHARACTERISTICS:
LENGTH: 3989 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 359:
US-09-070-927A-359
Query Match 16.5%; Score 44; DB 9; Length 3989;
Best Local Similarity 100.0%; Pred. No. 4,7e-14;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3627 GAAGATACACCTGTCCATGCCGAACACAGAGTTAAGCTTC 3584

RESULT 2

US-09-070-927A-550/c
; Sequence 550, Application US/09070927A
; Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Steven Barash
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 550:
SEQUENCE CHARACTERISTICS:
LENGTH: 9797 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 550:
US-09-070-927A-550
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Best Local Similarity 100.0%; Pred. No. 4,7e-14;
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; Sequence 345, Application US/09070927A
; Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Steven Barash
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:18:54 | Search time 113.856 Seconds
(without alignments)
1666.850 Million cell updates/sec

Title: US-10-088-666-1
Perfect score: 267
Sequence: 1 tatatcgaagtaagaccctc.....agtagctg99gagtcgcccc 267

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Gapop 60.0, Gapext 60.0

Searched: 824507 seqs, 35394441 residues

Word size: 10

Total number of hits satisfying chosen parameters: 100240

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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84	35	13.1	400	4 US-08-781-986A-3924	Sequence 3924, Ap
85	35	13.1	400	4 US-08-781-986A-4029	Sequence 4029, Ap
86	35	13.1	400	4 US-08-956-171E-4326	Sequence 4326, Ap
87	35	13.1	401	4 US-08-956-171E-4342	Sequence 4342, Ap
88	35	13.1	401	4 US-08-781-986A-4326	Sequence 4326, Ap
89	35	13.1	425	4 US-08-956-171E-3714	Sequence 3714, Ap
90	35	13.1	425	4 US-08-956-171E-3715	Sequence 3715, Ap
91	35	13.1	425	4 US-08-956-171E-3757	Sequence 3757, Ap
92	35	13.1	458	4 US-08-781-986A-3757	Sequence 3757, Ap
93	35	13.1	458	4 US-08-781-986A-3821	Sequence 3821, Ap
94	35	13.1	475	4 US-08-781-986A-3621	Sequence 3621, Ap
95	35	13.1	587	4 US-08-956-171E-3554	Sequence 3554, Ap
96	35	13.1	587	4 US-08-781-986A-3554	Sequence 3554, Ap
97	35	13.1	596	4 US-08-956-171E-3596	Sequence 3596, Ap
98	35	13.1	596	4 US-08-781-986A-3596	Sequence 3596, Ap
99	35	13.1	840	4 US-08-956-171E-508	Sequence 508, Ap
100	35	13.1	840	4 US-08-781-986A-508	Sequence 508, Ap

ALIGNMENTS

RESULT 1

US-09-134-000C-3148
Sequence 3148, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3148
LENGTH: 249
TYPE: DNA
ORGANISM: Enterococcus faecalis
US-09-134-000C-3148

Query Match 16.5%; Score 44; DB 4; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.8e-14;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 GAAGATACACCTGTTCCATGCCGACACAGAGTTAGCTTC 236
DB 48 GAAGATACACCTGTTCCATGCCGACACAGAGTTAGCTTC 91

RESULT 2

US-08-956-171E-5036/C
Sequence 5036, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Farnon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5236
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248PI

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1124
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 5036:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5036:
US-08-956-171E-5036

Query Match 13.1%; Score 35; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 ACACCTGTTCCATGCCGACACAGAGTTAGCT 234
DB 52 ACACCTGTTCCATGCCGACACAGAGTTAGCT 18

RESULT 3

US-08-781-986A-5036/C
Sequence 5036, Application US/08781986A
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5036:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-5036

Query Match 13.1%; Score 35; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 200 ACACCTGTTCCATGCCGACACAGAGTTAGCT 234
DB 52 ACACCTGTTCCATGCCGACACAGAGTTAGCT 18

RESULT 4

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:59:59 ; Search time 517.162 Seconds
(without alignments)
2710.166 Million cell updates/sec

Title: US-10-088-666-1

Perfect score: 267
Sequence: 1 tatatgaagtaagaccctt.....agtagtgggggacgcccc 267

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 413486 seqs, 2624710521 residues

Word size: 10

Total number of hits satisfying chosen parameters: 703887

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : N_Geneseq_23sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	267	100.0	267	5	AAFe1566	AAFe1566 Lactobaci
2	73	27.3	326	5	AAFe1567	AAFe1567 Lactobaci
3	50	18.7	338	5	AAFe1570	AAFe1570 Lactobaci
4	50	18.7	351	5	AAFe1568	AAFe1568 Lactobaci
5	50	18.7	414	5	AAFe1569	AAFe1569 Lactobaci
6	44	16.5	249	10	ADH8563	ADH8563 Enterococ
7	44	16.5	3989	2	AAK13286	AAK13286 Enterococ
8	44	16.5	3989	6	ABS99091	ABS99091 Enterococ
9	44	16.5	9797	6	AAK13487	AAK13487 Enterococ
10	44	16.5	9797	6	ABS99282	ABS99282 Enterococ
11	44	16.5	22960	6	AAK13282	AAK13282 Enterococ
12	44	16.5	22960	6	ABS99077	ABS99077 Enterococ
13	44	16.5	110000	10	ADP77343_05	Continuation (6 of 6)
14	44	16.5	110000	10	ADP77343_07	Continuation (8 of 8)
15	44	16.5	110000	10	ADP77343_18	Continuation (19 of 19)
16	44	15.0	317	5	AAFe1572	AAFe1572 L. coryni
17	40	15.0	317	5	AAFe1571	AAFe1571 L. coryni
18	40	15.0	326	5	AAFe1575	AAFe1575 Pediococc
19	40	15.0	335	5	AAFe1574	AAFe1574 Pediococc
20	40	2942	6	5	AB154766	AB154766 Pediococc
21	35	13.1	54	2	AAV79347	AAV79347 Stephyloc

22	35	13.1	187	2	AAV78993 Stephyloc
23	35	13.1	216	2	AAV78900 Stephyloc
24	35	13.1	221	2	AAV78883 Stephyloc
25	35	13.1	235	2	AAV78847 Stephyloc
26	35	13.1	242	2	AAV78849 Stephyloc
27	35	13.1	283	2	AAV78771 Stephyloc
28	35	13.1	300	2	AAV78726 Stephyloc
29	35	13.1	309	2	AAV78637 Stephyloc
30	35	13.1	327	2	AAV78653 Stephyloc
31	35	13.1	330	2	AAV78635 Stephyloc
32	35	13.1	338	2	AAV78557 Stephyloc
33	35	13.1	340	2	AAV78506 Stephyloc
34	35	13.1	348	2	AAV78486 Stephyloc
35	35	13.1	361	2	AAV78258 Stephyloc
36	35	13.1	361	2	AAV78607 Stephyloc
37	35	13.1	367	2	AAV78370 Stephyloc
38	35	13.1	367	2	AAV78530 Stephyloc
39	35	13.1	370	2	AAV78581 Stephyloc
40	35	13.1	371	2	AAV78429 Stephyloc
41	35	13.1	386	2	AAV78375 Stephyloc
42	35	13.1	389	2	AAV78201 Stephyloc
43	35	13.1	400	2	AAV77942 Stephyloc
44	35	13.1	400	2	AAV77981 Stephyloc
45	35	13.1	400	2	AAV77986 Stephyloc
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63	35	13.1	401	2	AAV78042 Stephyloc
64	35	13.1	425	2	AAV78025 Stephyloc
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66	35	13.1	587	2	AAV77865 Stephyloc
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68	35	13.1	840	2	AAV74819 Stephyloc
69	35	13.1	1051	2	AAV77885 Stephyloc
70	35	13.1	1089	4	AAH54969 S. epider
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72	35	13.1	2209	2	AAV77863 Stephyloc
73	35	13.1	2662	4	AAH54970 S. epider
74	35	13.1	2725	4	AAH54148 S. epider
75	35	13.1	2869	4	AAH55038 S. epider
76	35	13.1	2912	10	ADBE1699 21S rRNA
77	35	13.1	3012	4	AAH54319 S. epider
78	35	13.1	3019	4	AAH54554 S. epider
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80	35	13.1	3030	4	AAH54552 S. epider
81	35	13.1	3232	4	AAH54853 S. epider
82	35	13.1	3305	4	AAH54792 S. epider
83	35	13.1	3332	4	AAH54919 S. epider
84	35	13.1	3405	4	AAH54539 S. epider
85	35	13.1	3608	4	AAH54395 S. epider
86	35	13.1	3625	4	AAH54294 S. epider
87	35	13.1	3656	4	AAH54375 S. epider
88	35	13.1	3732	4	AAH54394 S. epider
89	35	13.1	3845	4	AAH54156 S. epider
90	35	13.1	3937	4	AAH54408 S. epider
91	35	13.1	4106	4	AAH54320 S. epider
92	35	13.1	4346	4	AAH54338 S. epider
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ALIGNMENTS

61 TGAAGCGTGAAGCGGACGACIACIATATGGTGAAGACIATACCAAGI CAACTACGTAAGT 120

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:16:19 : Search time 1543.47 Seconds
(without alignments)
6303.600 Million cell updates/sec

Title: US-10-088-666-1
Perfect score: 267
Sequence: 1 tatatgaagtaagacccct.....agtagtcgggggacgcgcc 267

Scoring table: Oligo-MTC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 segs, 18219865908 residues

Word size: 10

Total number of hits satisfying chosen parameters: 6545258

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

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2: gb_est2:*
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9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	22	8.2	6499	8	BH771024 LMGtag74
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5	20	7.5	693	8	B2170405 CH230-369
6	20	7.5	830	8	B2076210 Lk51d10.
7	19	7.1	547	8	BH386373 AG-ND-123
8	19	7.1	586	8	BH823931 BACP2-D0
9	19	7.1	622	8	AQ779183 HS_3185_A
10	19	7.1	667	2	BH865729 BB865729
11	19	7.1	672	8	BH396985 AG-ND-137
12	19	7.1	696	2	BE113195 UI-R-BJ1-
13	19	7.1	703	8	BE133195 AG-ND-137
14	19	7.1	709	8	BH402869 AG-ND-140
15	19	7.1	754	8	BH399988 AG-ND-137
16	19	7.1	759	8	BH381434 AG-ND-137
17	19	7.1	800	5	BX881725 ENTG39TF
18	19	7.1	829	8	AZ540485 NDG39TF
19	19	7.1	877	8	CC141515 ETL32K2.
20	19	7.1	888	8	CG965204 MBEMD88TF
21	18	6.7	161	1	AA815431 a165a05.s
22	18	6.7	233	5	BQ466564 HT02011r
23	18	6.7	275	4	BM376623 EBem05_SQ
24	18	6.7	286	1	AV155185 AV155185

25	18	6.7	300	1	AJ480648
26	18	6.7	306	2	BB359579
27	18	6.7	309	2	BB16773
28	18	6.7	328	7	CO750077
29	18	6.7	338	1	AU112531
30	18	6.7	356	8	BH402056 AG-ND-119
31	18	6.7	360	1	AJ469080
32	18	6.7	360	1	AJ474156
33	18	6.7	360	1	AJ474753
34	18	6.7	379	8	AQ078388
35	18	6.7	398	2	BE103481
36	18	6.7	398	2	BE211444
37	18	6.7	407	8	AZ176707
38	18	6.7	413	1	AJ436048
39	18	6.7	417	7	CO750063
40	18	6.7	420	1	AJ469076
41	18	6.7	420	1	AJ469077
42	18	6.7	420	1	AJ469078
43	18	6.7	420	1	AJ474752
44	18	6.7	424	2	AM662006
45	18	6.7	426	1	AA815371
46	18	6.7	435	4	BI535214
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52	18	6.7	515	6	CB871365
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54	18	6.7	558	8	AZ216879
55	18	6.7	560	4	BG987436
56	18	6.7	562	2	AM510851
57	18	6.7	562	8	AQ247784
58	18	6.7	563	2	BE755776
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60	18	6.7	604	2	AM985312
61	18	6.7	607	7	CF668065
62	18	6.7	609	6	CB438313
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64	18	6.7	620	6	CB863479
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67	18	6.7	653	8	BH269565
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71	18	6.7	684	7	CK974516
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73	18	6.7	719	6	CB420267
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84	18	6.7	808	7	CK362822
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86	18	6.7	842	8	AZ683885
87	18	6.7	872	9	CG118408
88	18	6.7	894	7	CG149888
89	18	6.7	898	8	CO750445
90	18	6.7	898	7	BH133066
91	18	6.7	900	8	BH147215
92	18	6.7	903	8	BH136872
93	18	6.7	937	9	CG118407
94	18	6.7	943	8	AZ136157
95	18	6.7	959	9	CC609999
96	18	6.7	985	9	CC610004
97	18	6.7	1227	9	CG751219

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BB16773	BB16773
CO750077	KBFAE004P
AU112531	AU112531
BH402056	AG-ND-119
AJ469080	AJ469080
AJ474156	AJ474156
AJ474753	AJ474753
AQ078388	CIT-ASP-2
BE103481	UI-R-BX0-
BE211444	SO40512.Y
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CO750063	KBFAE004O
AJ469076	AJ469076
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BI535214	398595.MA
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BM098432	EBem08.SQ
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CF668065	RTCNT_34
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CB420267	593204.MA
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BZ192101	CH230-279
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CO750445	KBAE007C
BH133066	ENTPAC6TR
BH147215	ENTOP41TR
BH136872	ENTNAB2TR
CG118407	PUR0H73TB
AZ136157	SP 0169.A
CC609999	OGTIN26TH
CC610004	OGULH26TV
CG751219	P045-3-GI

98 6.7 1258 8 BH770957 LLMGtag68
 c 99 18 6.7 1344 9 AG031219
 100 17 6.4 112 9 CGS44484 CGS44484 OST141740

ALIGNMENTS

RESULT 1
 LOCUS BZ369094 793 bp DNA linear GSS 19-NOV-2002
 DEFINITION Cot100.1.2.D04 Maize Cot100 library Zea mays genomic, genomic
 survey sequence.

ACCESSION BZ369094
 VERSION BZ369094
 KEYWORDS GI:25122715

SOURCE
 ORGANISM

Ze mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
 AUTHORS Yuan.Y., Samignuel.P. and Bennetzen.J.L.
 JOURNAL 1 (bases 1 to 793)
 Title: High Cot sequence analysis of the maize genome
 Unpublished (2003)
 Contact: Bennetzen J.L.
 Department of Biological Sciences
 Purdue University
 Hansen 339F, Purdue University, West Lafayette, IN 47907, USA
 Tel: 765 494 4499
 Fax: 765 496 1496
 Email: maize@ilbo.bio.purdue.edu

Forward and reverse reads were assembled when significant overlap
 was detected.
 Seg primer: T7 and T3
 Class: shotgun.

FEATURES
 source location/Qualifiers

1..793
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /dev_stage="10 days seedling"
 /lab_host="PH10B"
 /clone_lib="Maize Cot100 library"
 /note="Organ: young leaves; Vector: pcr4TOPO; Maize
 genomic DNA was sheared to fragments averaging about 1.8
 kb, was denatured and then reassociated in 1 X SSC at
 65°C. After a given Cot value was reached, aliquots were
 run over a hydroxyapatite (HAP) column in order to
 separate single stranded DNA from double stranded DNA. The
 single stranded DNA was then converted to a double
 stranded form with one round of Klenow DNA polymerase
 treatment with random 9-mer primers. The double-stranded
 fragments were then further size-selected over an agarose
 gel and cloned into the PCR4 TOPO vector."

ORIGIN

Query Match 21.0%; Score 56; DB 8; Length 793;
 Best Local Similarity 100.0%; Freq. No. 1.4e-20;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 189 GCGTGAAGATACACCTGTTCCATGCGACAGAGAAATTAGCTTACGACGCC 244
 189 |||||
 DB 314 GCGTGAAGATACACCTGTTCCATGCGACAGAGAAATTAGCTTACGACGCC 369

RESULT 2
 LOCUS BH770998 3268 bp DNA linear GSS 01-MAY-2002
 DEFINITION LLMGtag721 MG1363 Random Sequence Tag Library Lactococcus lactis
 subsp. cremoris genomic, genomic survey sequence.
 ACCESSION BH770998

VERSION BH770998.1 GI:20373955
 KEYWORDS GSS.
 SOURCE Lactococcus lactis subsp. cremoris
 ORGANISM Lactococcus lactis subsp. cremoris
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Lactococcus.

REFERENCE
 AUTHORS Bolotin.A., Ehrlich.S.D. and Sorokin.A.
 TITLE Studies of genomes of dairy bacteria Lactococcus lactis
 JOURNAL Sci. Aliments (2002) In press
 COMMENT Contact: Sorokin A
 Genetique Microbienne

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 CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
 Tel: 33 1 34 65 25 16
 Fax: 33 1 34 65 25 21
 Email: sorokine@jouy.inra.fr
 best homologue in strain IL1403 is dnag (93%)
 Class: shotgun
 High quality sequence start: 30
 High quality sequence stop: 3240.
 Location/Qualifiers

FEATURES
 source

1..3268
 /organism="Lactococcus lactis subsp. cremoris"
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 /strain="MG1363"
 /sub_species="cremoris"
 /db_xref="taxon:1359"
 /clone_lib="MG1363 Random Sequence Tag Library"
 /note="Vector: pSGMW2; Site 1: SmaI; Library of
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 prepared by partial AulI digestion or by sonication."

ORIGIN

Query Match 8.2%; Score 22; DB 8; Length 3268;
 Best Local Similarity 100.0%; Freq. No. 0.51;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 68 TGGAGCGGACCGACTACTAATCG 89
 422 TGGAGCGGACCGACTACTAATCG 443

RESULT 3
 LOCUS BH771024 6499 bp DNA linear GSS 01-MAY-2002
 DEFINITION LLMGtag746 MG1363 Random Sequence Tag Library Lactococcus lactis
 subsp. cremoris genomic, genomic survey sequence.
 ACCESSION BH771024
 VERSION BH771024
 KEYWORDS GI:20373981

GSS.
 Lactococcus lactis subsp. cremoris
 Lactococcus lactis subsp. cremoris
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Lactococcus.
 1 (bases 1 to 6499)
 Bolotin.A., Ehrlich.S.D. and Sorokin.A.
 Studies of genomes of dairy bacteria Lactococcus lactis
 Sci. Aliments (2002) In press
 Contact: Sorokin A
 Genetique Microbienne

INRA
 CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
 Tel: 33 1 34 65 25 16
 Fax: 33 1 34 65 25 21
 Email: sorokine@jouy.inra.fr
 best homologue in strain IL1403 is ywga (78%)
 Class: shotgun
 High quality sequence start: 30
 High quality sequence stop: 6471.
 Location/Qualifiers

1..6499
 /organism="Lactococcus lactis subsp. cremoris"

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:16:19 ; Search time 115.616 Seconds
(without alignments)

6303.600 Million cell updates/sec

Title: US-10-088-666-74

Perfect score: 20

Sequence: 1 gagggagaagatctctat 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 segs, 18219855908 residues

Word size: 10

Total number of hits satisfying chosen parameters: 725526

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hnc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	ID	Description
C 1	19	95.0	613	4	B1508715
C 2	17	85.0	268	4	B1508715
C 3	17	85.0	268	4	B1508715
C 4	17	85.0	584	1	AU016700
C 5	17	85.0	696	1	BE113195
C 6	17	85.0	1025	9	CL452767
C 7	16	80.0	205	4	BF998912
C 8	16	80.0	262	8	ACQ471789
C 9	16	80.0	301	2	BA36559
C 10	16	80.0	409	1	AV540606
C 11	16	80.0	411	8	AZ232723
C 12	16	80.0	419	6	CB764501
C 13	16	80.0	425	1	AA317772
C 14	16	80.0	425	8	ACQ80424
C 15	16	80.0	442	9	CL658098
C 16	16	80.0	445	5	CB744432
C 17	16	80.0	454	6	BO832471
C 18	16	80.0	467	6	CB714203
C 19	16	80.0	468	1	AL046182
C 20	16	80.0	520	9	CE570119
C 21	16	80.0	531	6	CA630367
C 22	16	80.0	542	4	BJ249708
C 23	16	80.0	573	9	CE251105
C 24	16	80.0	575	2	BF483725

C 25	16	80.0	581	8	AZ982290
C 26	16	80.0	590	4	BM704665
C 27	16	80.0	595	6	CB177816
C 28	16	80.0	607	4	BJ567993
C 29	16	80.0	607	6	CB634129
C 30	16	80.0	620	8	BX254803
C 31	16	80.0	635	8	AZ384762
C 32	16	80.0	650	4	BI113486
C 33	16	80.0	658	7	CN305165
C 34	16	80.0	662	5	BO829603
C 35	16	80.0	667	6	CB840482
C 36	16	80.0	671	5	BX918106
C 37	16	80.0	672	6	CB841003
C 38	16	80.0	682	9	AG235673
C 39	16	80.0	706	4	BI221782
C 40	16	80.0	730	8	AZ342561
C 41	16	80.0	737	9	AG422832
C 42	16	80.0	748	4	BG921699
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C 50	16	80.0	982	5	BO950615
C 51	15	75.0	82	6	CD838172
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C 53	15	75.0	150	5	BX511574
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C 82	15	75.0	231	2	BB435513
C 83	15	75.0	231	2	BB435571
C 84	15	75.0	231	2	BB435580
C 85	15	75.0	232	2	BB435218
C 86	15	75.0	232	2	BB435337
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CB841003	M15E-1452
AG235673	Mus muscu
BI221782	602937040
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AG422832	Mus muscu
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CO397391	ACENCCURT
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C 99 15 75.0 253 2 BB435379
C 100 15 75.0 253 2 BB436103

ALIGNMENTS

RESULT 1
BI508715/c 613 bp mRNA linear EST 08-APR-2002
LOCUS BI170011A10G03.5 Bee Brain Normalized/Subtracted Library, B17 Apis
DEFINITION mellifera cDNA clone BI170011A10G03 5', mRNA sequence.

ACCESSION BI508715
VERSION BI508715.1 GI:15359089
KEYWORDS Apis mellifera (honey bee)
SOURCE Apis mellifera
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygora;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apoidea; Apis

REFERENCE

1 (bases 1 to 613)
Whitfield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L.,
Pardines,J., Robertson,M.M., Soares,B. and Robinson,G.E.
Annotated expressed sequence tags and cDNA microarrays for studies
of brain and behavior in the honey bee
Genome Res. 12 (4), 555-566 (2002)

JOURNAL
MEDLINE
PUBMED

21929762
11932240

Contact: Gene E. Robinson
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University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel. 217 265 0308
Fax: 217 244 3499

Email: gene@life.uiuc.edu

This research was funded by the University of Illinois Critical
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
Award in Functional Genomics to G.E. Robinson and an NSF
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.

PCR Primers

FORWARD: TAATGACACTCATTATGCG
BACKWARD: ATTAACTCTCCTAAG

Plate: BI170011A10 row: G column: 03
Seq primer: AGCGATACCAATTCACACAGA

High quality sequence stop: 613.

FEATURES

source

1..613
Location/Qualifiers
/organism="Apis mellifera"
/mol_type="mRNA"
/strain="mixed strains of European bees, predominantly
A.m. ligustica"
/db_xref="taxon:7460"
/clone="BI170011A10G03"
/sex="female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
/clone_lib="Bee Brain Normalized/Subtracted Library, B17"
/note="Organ: brain; Vector: pRT73-Pac; Site 1: EcoRI;
Site 2: NotI; This B17 cDNA library was generated by
subtraction of the B16 library with 4000 previously
sequenced clones. The B16 library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. RNA was
prepared from dissected brains of adult worker bees of
various ages and various behavioral groups."

ORIGIN

Query Match 95.0%; Score 19; DB 4; Length 613;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAGAAAGTTCTTAT 20
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Db 573 AGGAGAAAGTTCTTAT 555

RESULT 2
BB434970/c

LOCUS BB434970 268 bp mRNA linear EST 01-AUG-2000
DEFINITION BB434970 RIKEN full-length enriched, adult pancreas islet cells Mus
musculus cDNA clone C820010E15 3', mRNA sequence.

ACCESSION BB434970
VERSION BB434970.1 GI:9274697
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 268)
Kanno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Horii,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadoya,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Sugahara,Y., Suzuki,H., Tagawa,A.,
Takanashi,F., Tomimaga,N., Toyota,T., Tsunoda,Y., Watabiki,A.,
Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
Hayashizaki,Y.
RIKEN Mouse ESTs (Kanno,H., et al.)
Unpublished (2000)

TITLE
JOURNAL
COMMENT

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Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermocatalytic activation of enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitanai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)

Please visit our web site (<http://genome.riken.go.jp>) for
further details.

FEATURES

source

1..268
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="C820010E15"
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/clone_lib="RIKEN full-length enriched, adult pancreas
islet cells"

/note="Site 1: SalI; Site 2: BamHI. cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:28:49 ; Search time 34.4144 Seconds
(without alignments) updates/sec
3138.794 Million cell

Title: US-10-088-666-74

Perfect score: 20
Sequence: 1 gaggaagaagttctctat 20

Scoring table: OLIGO_NUC,
Gapop 60.0, Gapext 60.0

Searched: 3625171 seqs, 2700493622 residues

Word size: 10

Total number of hits satisfying chosen parameters: 95006

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

Published Applications NA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	80.0	688	13	US-10-027-632-102171	Sequence 102171, A
5	80.0	688	15	US-10-027-632-102170	Sequence 102170, A
6	80.0	688	15	US-10-027-632-102171	Sequence 102171, A
7	80.0	2022	17	US-10-437-963-57769	Sequence 57769, A
8	80.0	6109	10	US-09-795-061-1	Sequence 1, Appli
9	80.0	6200	10	US-09-795-061-3	Sequence 3, Appli
10	80.0	6337	15	US-10-369-493-25224	Sequence 25224, A
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13	75.0	448	16	US-10-425-114-12489	Sequence 12489, A
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16	75.0	539	10	US-09-814-353-9722	Sequence 9722, App
17	75.0	571	14	US-10-219-220-247	Sequence 247, App
18	75.0	605	9	US-09-938-842A-4989	Sequence 4989, App
19	75.0	1166	14	US-09-938-842A-4989	Sequence 4989, App
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21	75.0	1284	17	US-10-437-963-52109	Sequence 52109, A
22	75.0	1284	17	US-10-437-963-52109	Sequence 52109, A
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34	75.0	4414	10	US-09-845-416-32	Sequence 32, Appli
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38	75.0	4848	10	US-09-845-416-35	Sequence 35, Appli
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52	75.0	13957	15	US-10-149-736-1	Sequence 1, Appli
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54	75.0	14069	16	US-10-342-887-434	Sequence 434, App
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56	75.0	14082	15	US-10-172-118-981	Sequence 981, App
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61	75.0	175561	16	US-10-235-192A-48	Sequence 48, Appli
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ALIGNMENTS

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; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 45008
; LENGTH: 465
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; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_141051C.1
US-10-425-115-45008

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; Sequence 797, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
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; TYPE: DNA
; ORGANISM: Mus musculus
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; LOCATION: (1)-(127767)
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Best Local Similarity 100.0%; Pred. No. 4.3;
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; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
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; Sequence 102171, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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17	14	70.0	3880	4	US-09-221-017B-1071
18	14	70.0	4053	4	US-09-620-312D-156
19	14	70.0	4519	3	US-08-976-289-6
20	14	70.0	4519	4	US-09-956-004-6
21	14	70.0	4948	4	US-09-562-702A-23
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23	14	70.0	4872	4	US-09-562-702A-27
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; Sequence 1, Application US/09795061
; Patent No. 6795528
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S
; APPLICANT: Imamura, Yasutada
; TITLE OF INVENTION: Pro-Alpha 3 (V) Collagen Genes
; FILE REFERENCE: 960296.96781
; CURRENT APPLICATION NUMBER: US/09/795,061
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6109
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)..(5298)
US-09-795-061-1
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Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Patent No. 6795528
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S
; APPLICANT: Imamura, Yasutada
; TITLE OF INVENTION: Pro-Alpha 3 (V) Collagen Genes
; FILE REFERENCE: 960296.96781
; CURRENT APPLICATION NUMBER: US/09/795,061
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 6200
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (87)..(5321)
US-09-795-061-3
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Query Match      80.0%; Score 16; DB 4; Length 6200;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GAGGAGAGAGTCTTC 16
      |||
      4927 GAGGAGAGAGTCTTC 4942
```

```
RESULT 3
US-09-325-932A-139/c
; Sequence 139, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
```

```
; APPLICANT: Iasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 139
; LENGTH: 1166
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-325-932A-139
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Query Match      75.0%; Score 15; DB 4; Length 1166;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      6 AAGAGTCTCTTAT 20
      |||
      1001 AAGAGTCTCTTAT 987
```

RESULT 4

```
US-09-687-875A-1/c
; Sequence 1, Application US/09687875A
; Patent No. 6544786
; GENERAL INFORMATION:
; APPLICANT: Xiao, Xiao
; APPLICANT: Liu, Paul
; TITLE OF INVENTION: METHOD AND VECTOR FOR PRODUCING AND TRANSFERRING TRANS-SPICED PE
; FILE REFERENCE: 00792
; CURRENT APPLICATION NUMBER: US/09/687,875A
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/158,868
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 5952
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2897)..(2898)
; OTHER INFORMATION: S4 junction site
; NAME/KEY: misc feature
; LOCATION: (3198)..(3199)
; OTHER INFORMATION: S2 junction site
US-09-687-875A-1
```

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Query Match      75.0%; Score 15; DB 4; Length 5952;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 GGGAGAGAGTCTCT 17
      |||
      874 GGGAGAGAGTCTCT 860
```

```
RESULT 5
US-09-484-970B-60/c
; Sequence 60, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkuth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:59:59 ; Search time 38.7387 Seconds
(without alignments)
2710.166 Million cell updates/sec

Title: US-10-088-666-74

Perfect score: 20

Sequence: 1 gagggagaagatctcttcat 20

Scoring table: OLIGO_NUC;
Gapop 60.0, Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size: 10

Total number of hits satisfying chosen parameters: 88295

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

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1: geneseqn1980s:*
2: geneseqn1900s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	5	AA61639 Lactobac
2	20	100.0	267	5	AA61639 Lactobac
3	16	80.0	337	6	ABN26443 Human ORF
4	16	80.0	995	10	ADK53632 Plant DNA
5	16	80.0	995	10	ADK55905 Plant DNA
6	16	80.0	6109	4	AAH78667 Murine CO
7	16	80.0	6200	4	AAH78667 Murine CO
8	16	80.0	6200	12	ADQ19840 Human COL
9	16	80.0	6368	6	ABN59647 Novel hum
10	16	80.0	6617	12	ADQ23958 Human sof
11	15	75.0	255	6	ABK81965 Human dys
12	15	75.0	445	2	AA91154 Strawber
13	15	75.0	500	6	ABQ63274 Genomic a
14	15	75.0	535	3	AA52735 Arabidops
15	15	75.0	539	5	AD170662 Human cya
16	15	75.0	539	5	AD170662 Human cya
17	15	75.0	571	10	ADB94883 Programme
18	15	75.0	605	6	AB217884 Arabidops
19	15	75.0	661	2	AA91127 Strawberry
20	15	75.0	702	2	AA92053 DNA encod
21	15	75.0	1034	2	AAQ06255 Glucagon-

22	15	75.0	1034	2	AA773216 Rat prepr
23	15	75.0	1034	2	AA220678 Preproglu
24	15	75.0	1166	4	AA44834 RPP5-Like
25	15	75.0	1166	10	ADB94775 Programme
26	15	75.0	1340	6	AAAD37233 Human dys
27	15	75.0	1667	6	AAAD37235 Human dys
28	15	75.0	1991	6	AAAD37231 Human dys
29	15	75.0	2230	3	AAAC54329 Arabidops
30	15	75.0	3446	3	AA248570 A rod sho
31	15	75.0	3510	6	AAAD37242 Human dys
32	15	75.0	3531	6	AAAD37238 Human dys
33	15	75.0	3747	3	AA248566 A rod sho
34	15	75.0	3858	6	AAAD37237 Human dys
35	15	75.0	3999	6	AAAD37234 Human dys
36	15	75.0	4075	3	AA248569 A rod sho
37	15	75.0	4182	3	AAAD37230 Human dys
38	15	75.0	4402	3	AA248568 A rod sho
39	15	75.0	4402	3	AA248567 A rod sho
40	15	75.0	4414	6	AAAD37260 Adeno-ass
41	15	75.0	4476	6	AAAD37259 Adeno-ass
42	15	75.0	4476	6	AAAD37258 Adeno-ass
43	15	75.0	4825	6	AAAD37257 Adeno-ass
44	15	75.0	4848	6	AAAD37263 Adeno-ass
45	15	75.0	4966	6	AAAD37256 Adeno-ass
46	15	75.0	4990	6	AAAD37262 Adeno-ass
47	15	75.0	5060	6	AAAD37264 Adeno-ass
48	15	75.0	5149	6	AAAD37255 Adeno-ass
49	15	75.0	5268	5	ABAI7929 Human ner
50	15	75.0	5339	6	ABK81998 DNA encod
51	15	75.0	5417	6	ABK81997 DNA encod
52	15	75.0	5462	6	ABK81999 DNA encod
53	15	75.0	5952	5	AAAD6794 Human dys
54	15	75.0	6798	5	ABAI5941 Human ner
55	15	75.0	6798	5	ABAI5941 Human ner
56	15	75.0	11068	6	ABK82000 DNA encod
57	15	75.0	11241	6	ABK82005 DNA encod
58	15	75.0	11443	6	ABK82002 DNA encod
59	15	75.0	12923	1	AAAN90338 Sequence
60	15	75.0	13957	6	ABK81959 DNA encod
61	15	75.0	13957	6	ABK81959 DNA encod
62	15	75.0	13957	6	ABK81959 DNA encod
63	15	75.0	13957	6	ABK81959 DNA encod
64	15	75.0	13957	6	ABK81959 DNA encod
65	15	75.0	13977	6	ABK81959 DNA encod
66	15	75.0	13977	6	ABK81959 DNA encod
67	15	75.0	14069	12	ADN04003 Antipso
68	15	75.0	21082	5	ABAI7928 Human ner
69	15	75.0	21087	5	ABAI7927 Human ner
70	15	75.0	21989	5	ABAI5942 Human ner
71	15	75.0	110000	2	AAK91980_04
72	15	75.0	17561	8	AAAD5694 Human THB
73	15	75.0	17561	8	AAAD5694 Human THB
74	15	75.0	214019	10	ADL08129 Human gen
75	15	75.0	273254	3	AAAC81914 Chlamydia
76	15	75.0	25	3	AAAC16287 Human mic
77	15	75.0	32	2	AAAB92382 Galatins
78	15	75.0	225	3	AAAC48437 Arabidops
79	15	75.0	227	4	AAH06218 Human CDN
80	15	75.0	257	10	ADB94774 Programme
81	15	75.0	276	6	ABL173526 Corn tass
82	15	75.0	309	2	AAV90247 EST clone
83	15	75.0	324	8	ACD05660 cDNA encod
84	15	75.0	333	12	ADJ44398 Plant CDN
85	15	75.0	433	4	AAH06218 Human CDN
86	15	75.0	559	2	AAV8761 EST clone
87	15	75.0	575	12	ACH74438 Human gen
88	15	75.0	579	10	ADJ56276 Human CDN
89	15	75.0	599	5	AAH88772 Alpha-glu
90	15	75.0	615	8	AAH88772 Alpha-glu
91	15	75.0	636	3	AAAF08357 Fusarium
92	15	75.0	675	3	AAAO1777 Human col
93	15	75.0	768	4	AAAF5636 H. pylori
94	15	75.0	822	10	AD607722 Novel cod

95	14	70.0	831	5	AA888057	DNA	encod
96	14	70.0	831	5	AA864236	DNA	encod
97	14	70.0	856	6	ABQ44964	Oligonuci	
98	14	70.0	856	6	ABQ44965	Oligonuci	
99	14	70.0	858	10	ADC91032	E. faeciu	
100	14	70.0	1122	11	ABD14125	Pseudomon	

ALIGNMENTS

RESULT 1

AA61639

ID AA61639 standard; DNA; 20 BP.

AA61639;

02-JUL-2001 (first entry)

Lactobacillus brevis 23S rRNA/5S rRNA specific probe SEQ ID 74.

23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.

Lactobacillus brevis.

DE19945964-A1.

05-APR-2001.

24-SEP-1999; 99DE-01045964.

24-SEP-1999; 99DE-01045964.

(BIOT-) BIOTECON DIAGNOSTICS GMBH.

Fandke M, Gasch A, Berghof K;

WPI; 2001-246136/26.

Detecting contaminating microorganisms in brewing, by nucleic acid amplification and hybridization, either non-specific or genus- or species specific.

Claim 9(i); Page 17; 48pp; German.

This invention describes a novel method for detecting microorganisms (A) of importance in brewing which comprises treating a sample with at least two primers (P1) that hybridize to a consensus region in the nucleic acid of (A), at least part of the microbial nucleic acid is amplified, the amplicon is treated with at least one probe (P2) that hybridizes specifically with a sequence common to all (A) or specific for one or more families, genera or species, and any formation of hybrids is detected. The method is used to detect, identify and/or characterize microorganisms in beer or brewing materials, particularly for detecting contamination. The method may detect the entire range of contaminating microbes, either as a general test for contamination or as a test specific for particular genera or (sub)species. It is quicker than known microbiological methods, and can detect several organisms in the same sample, including organisms not presently recognized as contaminants. The method provides an early indication of contamination and can be automated for high throughput analysis

Sequence 20 BP; 6 A; 2 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 5; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGGAAGAAGTCTCTTAT 20

DB 1 GAGGGAAGAAGTCTCTTAT 20

RESULT 2

AA61566

ID AA61566 standard; DNA; 267 BP.

AA61566;

02-JUL-2001 (first entry)

Lactobacillus brevis 23S rRNA-spacer-5S rRNA DNA fragment.

23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.

Lactobacillus brevis.

DE19945964-A1.

05-APR-2001.

24-SEP-1999; 99DE-01045964.

24-SEP-1999; 99DE-01045964.

(BIOT-) BIOTECON DIAGNOSTICS GMBH.

Fandke M, Gasch A, Berghof K;

WPI; 2001-246136/26.

Detecting contaminating microorganisms in brewing, by nucleic acid amplification and hybridization, either non-specific or genus- or species specific.

Claim 9(i); Page 9; 48pp; German.

This invention describes a novel method for detecting microorganisms (A) of importance in brewing which comprises treating a sample with at least two primers (P1) that hybridize to a consensus region in the nucleic acid of (A), at least part of the microbial nucleic acid is amplified, the amplicon is treated with at least one probe (P2) that hybridizes specifically with a sequence common to all (A) or specific for one or more families, genera or species, and any formation of hybrids is detected. The method is used to detect, identify and/or characterize microorganisms in beer or brewing materials, particularly for detecting contamination. The method may detect the entire range of contaminating microbes, either as a general test for contamination or as a test specific for particular genera or (sub)species. It is quicker than known microbiological methods, and can detect several organisms in the same sample, including organisms not presently recognized as contaminants. The method provides an early indication of contamination and can be automated for high throughput analysis

Sequence 267 BP; 77 A; 51 C; 77 G; 62 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 5; Length 267;

Best Local Similarity 100.0%; Pred. No. 0.29;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGGAAGAAGTCTCTTAT 20

DB 154 GAGGGAAGAAGTCTCTTAT 173

RESULT 3

ABN26443

ID ABN26443 standard; cDNA; 337 BP.

ABN26443;

24-JUN-2002 (first entry)

Human ORFX polymucleotide sequence SEQ ID NO:21363.

Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 12:43:29 ; Search time 156.156 Seconds
(without alignments)

6056.719 Million cell updates/sec

Title: US-10-088-666-74

Perfect score: 20
Sequence: 1 gagggaagaagtcctctat 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4526729 segs, 23544849745 residues

Word size: 10

Total number of hits satisfying chosen parameters: 353379

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_rts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	AX105802	Sequence
2	20	100.0	267	AX105729	Sequence
3	18	90.0	229813	AC117613	Mus muscu
4	17	85.0	101707	AC150157	Gallus ga
5	17	85.0	128809	AC021648	Homo sapi
6	17	85.0	172825	AC020614	Homo sapi
7	17	85.0	187221	AC117229	Mus muscu
8	17	85.0	192734	AL928798	Mouse DNA
9	17	85.0	192944	AC146902	Callicebu
10	17	85.0	227515	AC150065	Gallus ga
11	17	85.0	234651	AC115456	Rattus no
12	16	80.0	337	CQ455803	Sequence
13	16	80.0	1473	AY039654	Danio rer
14	16	80.0	1907	CQ723784	Sequence
15	16	80.0	2638	RABMB4	rabbit embr
16	16	80.0	6076	AF272661	Rattus no
17	16	80.0	6109	AX239611	Sequence
18	16	80.0	6109	AF176645	Mus muscu
19	16	80.0	6200	AX239613	Sequence

20	16	80.0	6200	9	AF177941	Homo sapi
21	16	80.0	6368	8	AX405643	Sequence
22	16	80.0	7374	6	SCCDC	X70151 S. cerevisi
23	16	80.0	44594	4	RABRGLOR	M18818 Rabbit beta
24	16	80.0	72872	8	FL104	AF096370 Arabidops
25	16	80.0	76425	9	AC105346	AC105346 Homo sapi
26	16	80.0	105907	2	AC026429	Homo sapi
27	16	80.0	110000	1	EX908798	Continuation (2 of
28	16	80.0	110000	2	AC116152_2	Continuation (3 of
29	16	80.0	110000	2	AC149068_0	Continuation (3 of
30	16	80.0	112945	8	AC027683	AC027683 Homo sapi
31	16	80.0	135785	8	AC051634	AC051634 Oryza sat
32	16	80.0	141773	2	AC069348	AC069348 Homo sapi
33	16	80.0	141790	10	AL671759	AL671759 Mouse DNA
34	16	80.0	144207	2	AC115887	AC115887 Mus muscu
35	16	80.0	150872	8	AP003574	AP003574 Oryza sat
36	16	80.0	153616	2	AC136945	AC136945 Homo sapi
37	16	80.0	156054	9	HSDJ16705	AL121938 Human DNA
38	16	80.0	156791	9	HSDJ56094	AL045594 Human DNA
39	16	80.0	158756	2	AC137793	AC137793 Homo sapi
40	16	80.0	163757	2	AC141448	AC141448 Homo sapi
41	16	80.0	165500	9	AC093784	AC093784 Homo sapi
42	16	80.0	167231	9	AC099571	AC099571 Homo sapi
43	16	80.0	169765	9	AC006075	AC006075 Homo sapi
44	16	80.0	170106	9	AC104371	AC104371 Homo sapi
45	16	80.0	176625	8	AP004992	AP004992 Oryza sat
46	16	80.0	177029	2	AC079079	AC079079 Homo sapi
47	16	80.0	178366	2	AC142217	AC142217 Rattus no
48	16	80.0	178397	2	AC131789	AC131789 Mus muscu
49	16	80.0	183067	9	AC040914	AC040914 Homo sapi
50	16	80.0	183583	9	AC068408	AC068408 Homo sapi
51	16	80.0	184909	9	AL356057	AL356057 Human DNA
52	16	80.0	189616	2	AC121093	AC121093 Mus muscu
53	16	80.0	189628	2	AC146318	AC146318 Gallus ga
54	16	80.0	198697	8	ATCRRIV4	AL161492 Arabidops
55	16	80.0	198788	8	ATCRRIV46	AL161546 Arabidops
56	16	80.0	199825	9	AC099570	AC099570 Homo sapi
57	16	80.0	200891	2	AC106816	AC106816 Mus muscu
58	16	80.0	202576	10	AC140931	AC140931 Mus muscu
59	16	80.0	207674	8	ATFCB8	297343 Arabidops
60	16	80.0	212437	2	AC139865	AC139865 Mus muscu
61	16	80.0	218632	2	AC138333	AC138333 Mus muscu
62	16	80.0	220313	2	AC145406	AC145406 Gallus ga
63	16	80.0	221478	2	AC079545	AC079545 Mus muscu
64	16	80.0	222159	2	AC106540	AC106540 Rattus no
65	16	80.0	229114	2	AC106554	AC106554 Rattus no
66	16	80.0	234182	2	AC111393	AC111393 Rattus no
67	16	80.0	234862	2	AC131024	AC131024 Rattus no
68	16	80.0	238147	3	CNS07EGF	AL590448 chromosom
69	16	80.0	245671	2	AC112762	AC112762 Rattus no
70	16	80.0	247462	2	AC134478	AC134478 Rattus no
71	16	80.0	258445	2	AC126131	AC126131 Rattus no
72	16	80.0	261665	2	AC095565	AC095565 Rattus no
73	16	80.0	267520	2	AC095489	AC095489 Rattus no
74	16	80.0	300029	8	AE011113	AE011113 Oryza sat
75	16	80.0	316613	1	SCCHR11	AY59720 S. cerevisia
76	16	75.0	173	1	AY434428	AY434428 Unculture
77	15	75.0	255	6	AX538587	AX538587 Sequence
78	15	75.0	334	9	AF213405	AF213405 Homo sapi
79	15	75.0	385	1	AF078273	AF078273 Grassland
80	15	75.0	414	1	AF078284	AF078284 Grassland
81	15	75.0	428	1	AY214627	AY214627 Unculture
82	15	75.0	445	1	AF365745	AF365745 Unculture
83	15	75.0	445	6	AF64103	AF64103 Sequence
84	15	75.0	445	6	AY785039	AY785039 Sequence
85	15	75.0	468	1	UBA421881	UBA421881 Unculture
86	15	75.0	500	6	AX474829	AX474829 Sequence
87	15	75.0	509	10	RATGLD6	K02813 Rat glucago
88	15	75.0	535	8	AY084318	AY084318 Arabidops
89	15	75.0	539	6	CQ396333	CQ396333 Sequence
90	15	75.0	539	6	CQ402651	CQ402651 Sequence
91	15	75.0	553	1	AF432751	AF432751 Unculture
92	15	75.0	605	6	AX510294	AX510294 Sequence

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:16:19 ; Search time 144.52 seconds
(without alignments)
6303.600 Million cell updates/sec

Title: US-10-088-666-73

Perfect score: 25

Sequence: 1 tcgagataatcgataatcctag 25

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size: 10

Total number of hits satisfying chosen parameters: 675855

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Listing first 100 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	76.0	877	8	CG141515
2	19	76.0	888	9	CG965204
3	18	72.0	668	7	CR286805
4	18	72.0	738	7	CR286927
5	18	72.0	797	8	BZ192101
6	18	72.0	808	7	CK362822
7	18	72.0	848	8	AZ683885
8	18	72.0	898	8	BH133066
9	18	72.0	900	8	BH147215
10	18	72.0	903	8	BH136872
11	18	72.0	1227	9	CG751219
12	17	68.0	407	8	AZ176707
13	17	68.0	458	8	AZ177785
14	17	68.0	506	9	CG696733
15	17	68.0	512	8	AZ955016
16	17	68.0	513	8	AQ382746
17	17	68.0	513	9	CR758285
18	17	68.0	519	9	CR256503
19	17	68.0	534	8	AQ819623
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41	17	68.0	745	8	CE770220
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44	17	68.0	786	7	CK026066
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ALIGNMENTS

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LOCUS CC141515 877 bp DNA linear GSS 16-APR-2003
DEFINITION NDL.32K2.SP6 Notre Dame Liverpool Aedes aegypti genomic clone
CC141515 NDL.32K2, genomic survey sequence.
ACCESSION CC141515
VERSION CC141515.1 GI:30010570
KEYWORDS GSS.
SOURCE Aedes aegypti (yellow fever mosquito)
ORGANISM Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes;
Stegomyia.

REFERENCE 1 (bases 1 to 877)
AUTHORS Loftus,B., Shetty,J., Knudson,D. and Severson,D.
TITLE BAC end sequencing of Aedes aegypti
JOURNAL Unpublished (2003)
COMMENT Other GSSs: NDL.32K2.T7
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by David Severson
Seq primer: SP6
Class: BAC ends.

FEATURES

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Best Local Similarity 100.0%; Pred. No. 2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 GAATAATGATATATCT 23
DB 575 GAATATTTGATATATCT 593

RESULT 2
LOCUS CG965204 888 bp DNA linear GSS 15-DEC-2003
DEFINITION M8EMD88TRF.mth2 Medicago truncatula genomic clone 84P8, genomic survey sequence.
ACCESSION CG965204
VERSION CG965204.1 GI:39890624
KEYWORDS GSS.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.

REFERENCE 1 (bases 1 to 888)
AUTHORS Town,C.D., Shetty,J., Koo,H. and Feldblum,T.F.
TITLE Sequencing of BAC ends from Medicago truncatula
JOURNAL Unpublished (2003)
COMMENT Other GSSs: M8EMD88TR
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
Seq primer: TGTATATACGACGGCCAGT
Class: BAC ends.

FEATURES

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 GAATAATGATATATCT 23
DB 129 GAATATTTGATATATCT 147

RESULT 3
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DEFINITION CR286805 Oryza sativa library (Han B) Oryza sativa cDNA clone
P720G0893, mRNA sequence.
ACCESSION CR286805
VERSION CR286805.1 GI:44673371
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 668)
AUTHORS Han,B., Feng,Q., Huang,Y.C., Yang,K., Li,Y., Guan,J.P., Zhu,J.J.,
Zhao,Q., Hu,X., Liu,Y.L., Ma,J., Yu,Z., Chen,L., Fan,D.L.,
Weng,Q.J., Zhang,L., Lu,Y.Q., Yu,S.L., Liu,X.H., Lu,T.T.,
Zhang,Y.J., Lu,Y., Li,C., Li,T., Zhang,Y., Hu,H., Jia,P.X.,
Zhang,L., Fan,L.F., Chen,W., Wu,S.A. and Xue,Y.B.

TITLE Rice cDNA EST clone
JOURNAL Unpublished (2003)
COMMENT Contact: Han Bin
National Center for Gene Research
Chinese Academy of Sciences
500# Cao Bao Road, Shanghai 200233, China
Email: bhanengr.ac.cn
Clone requests: bhanengr.ac.cn
This is rice cDNA est clone
Web site: http://www.ncgr.ac.cn.
location/Qualifiers

FEATURES

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ORIGIN

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c 93 15 60.0 2136 15 US-10-227-646-227 Sequence 227, App
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c 95 15 60.0 2311 17 US-10-437-963-6048 Sequence 6048, App
c 96 15 60.0 2581 16 US-10-429-949-187 Sequence 187, App
c 97 15 60.0 3001 15 US-10-147-603-187 Sequence 187, App
c 98 15 60.0 3005 18 US-10-425-115-52901 Sequence 52901, A
c 99 15 60.0 3519 16 US-10-282-122A-21681 Sequence 21681, A
c 100 15 60.0 3927 15 US-10-252-157-260 Sequence 260, App

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ALIGNMENTS

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RESULT 1
US-09-070-927A-714/C
; Sequence 714, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunach
; Patrick J. Dillon
; Steven Barash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070, 927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 714:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1190 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 714:
US-09-070-927A-714

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Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-437-963-45894/C
; Sequence 45894, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 45894
; LENGTH: 1891
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48814C.1
US-10-437-963-45894

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Query Match 72.0%; Score 18; DB 17; Length 1891;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1793 AATATTGATATAATCT 1776

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RESULT 3
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; Sequence 1259, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
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; LENGTH: 5962
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: 5264
; OTHER INFORMATION: n is a or g or c or t
US-10-311-455-1259

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:18:54 ; Search time 10.6607 Seconds

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1666.850 Million cell updates/sec

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Perfect score: 25

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size: 10

Total number of hits satisfying chosen parameters: 12495

Minimum DB seq length: 0

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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
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SUMMARIES

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6	15	60.0	492	4	US-09-621-976-18621
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8	15	60.0	572	4	US-09-529-360B-65
9	15	60.0	854	4	US-09-247-155-67
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C	66	14	56.0	6854	2	US-08-376-843-4	Sequence 759, Ap
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C	69	14	56.0	9072	4	US-08-956-171E-45	Sequence 45, Appl1
C	70	14	56.0	9072	4	US-08-781-986A-45	Sequence 45, Appl1
C	71	14	56.0	99500	3	US-09-798-096-10	Sequence 10, Appl1
C	72	14	56.0	128779	4	US-09-497-855A-38	Sequence 38, Appl1
C	73	14	56.0	640681	4	US-09-790-988-1	Sequence 1, Appl1
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C	76	14	56.0	1830121	4	US-10-329-960-1	Sequence 4, Appl1
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C	87	13	52.0	246	4	US-09-543-681A-2795	Sequence 2795, Ap
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ALIGNMENTS

RESULT 1

US-09-270-767-27323
 ; Sequence 27323, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 27323
 ; LENGTH: 183
 ; TYPE: DNA
 ; ORGANISM: Drosophila melanogaster
 ; US-09-270-767-27323

Query Match 64.0%; Score 16; DB 4; Length 183;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AATTGAATATATCTA 24
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 Db 85 AATTGAATATATCTA 100

RESULT 2

US-09-270-767-11703
 ; Sequence 11703, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 11703
 ; LENGTH: 442
 ; TYPE: DNA
 ; ORGANISM: Drosophila melanogaster
 ; US-09-270-767-11703

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 Best Local Similarity 100.0%; Pred. No. 4.1;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AATTGAATATATCTA 24
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 Db 344 AATTGAATATATCTA 359

RESULT 3

US-09-248-796A-3349/c
 ; Sequence 3349, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstein et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO: 3349
 ; LENGTH: 1275
 ; TYPE: DNA
 ; ORGANISM: Candida albicans
 ; US-09-248-796A-3349

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 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 AATTGAATATATCTA 24
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 Db 203 AATTGAATATATCTA 188

RESULT 4

US-09-492-308A-3
 ; Sequence 3, Application US/09492308A
 ; Patent No. 6573430
 ; GENERAL INFORMATION:
 ; APPLICANT: Bradley, DJ
 ; Carpenter, R
 ; Coen, ES

TITLE OF INVENTION: Flowering genes
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon & Vanderhye PC
 STREET: 8th Floor, 1100 No. 6573430th Glebe Road
 CITY: Arlington
 STATE: Virginia
 COUNTRY: United States of America
 ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/492,308A
 FILING DATE: 27-Jan-2000
 CLASSIFICATION: 435 (Preliminary)

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/043,029
 FILING DATE: 13-MAR-1998
 APPLICATION NUMBER: PCT/GB96/02276
 FILING DATE: 13-SEP-1996
 APPLICATION NUMBER: GB 9518731.6
 FILING DATE: 13-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: Mary J. Wilson
 REGISTRATION NUMBER: 32,955
 REFERENCE/DOCKET NUMBER: 620-93
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 6527 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Antirrhinum majus
 IMMEDIATE SOURCE:
 CLONE: CEN GENOMIC
 POSITION IN GENOME:
 UNITS: bp

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-492-308A-3

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 12:43:29 ; Search time 195.195 Seconds
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Title: US-10-088-666-73

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Word size: 10

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Minimum DB seq length: 0
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Post-processing: Listing first 100 summaries

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14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	20	80.0	178448	9 AC099805	AC099805 Homo sapi
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6	19	76.0	119113	5 BX005139	BX005139 Zebrafish
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8	19	76.0	149163	2 AC073835	AC073835 Homo sapi
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11	19	76.0	226341	2 AC130020	AC130020 Rattus no
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15	18	72.0	1600	1 SHF19VEA	M33790 S.sonnei ce
16	18	72.0	1601	1 SFVIRB	X13340 Shigella fl
17	18	72.0	1937	1 SDIPAR	X63593 S.dysenter
18	18	72.0	5962	6 AX346188	AX346188 Sequence
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C 22	18	72.0	31998	1 AY206439	AY206439 Shigella
C 23	18	72.0	68808	2 AC022708	AC022708 Homo sapi
C 24	18	72.0	109321	9 AC021079	AC021079 Homo sapi
C 25	18	72.0	134651	8 AC145222	AC145222 Medicago
C 26	18	72.0	14601	8 AC104709	AC104709 Oryza sat
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C 30	18	72.0	169530	5 BX247907	BX247907 Zebrafish
C 31	18	72.0	181412	10 AC100154	AC100154 Mus muscu
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C 33	18	72.0	198491	2 AC022249	AC022249 Homo sapi
C 34	18	72.0	199548	8 ATCHRIV45	AL161545 Arabidops
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C 36	18	72.0	213494	1 SFPWR100	AL391753 Shigella
C 37	18	72.0	221618	1 AF348706	AF348706 Shigella
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C 44	17	68.0	12031	3 AF100660	AF100660 Caenorhab
C 45	17	68.0	23764	3 AC006723	AC006723 Caenorhab
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C 47	17	68.0	27514	8 AY344225	AY344225 Candida g
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C 53	17	68.0	86945	2 AC002490	AC002490 Homo sapi
C 54	17	68.0	88721	2 AC0021952	AC0021952 Mus muscu
C 55	17	68.0	93633	9 AL627317	AL627317 Human DNA
C 56	17	68.0	97631	2 AC141670	AC141670 Apis mell
C 57	17	68.0	108979	9 AC090041	AC090041 Homo sapi
C 58	17	68.0	110000	2 AC106777	AC106777 Homo sapi
C 59	17	68.0	110000	8 CR382138_17	CR382138_17 Cont
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C 61	17	68.0	134680	2 AC015726	AC015726 Homo sapi
C 62	17	68.0	141453	2 BX511307	BX511307 Danio rer
C 63	17	68.0	142978	9 AC097717	AC097717 Homo sapi
C 64	17	68.0	152177	10 AL672064	AL672064 Mouse DNA
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C 73	17	68.0	170355	9 AC026421	AC026421 Homo sapi
C 74	17	68.0	170585	2 AC127982	AC127982 Rattus no
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C 76	17	68.0	174622	9 AC104076	AC104076 Homo sapi
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 95 17 68.0 199326 2 AC120976
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 99 17 68.0 203737 10 AC116461
 100 17 68.0 208225 10 AC111022

ALIGNMENTS

RESULT 1
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 DEFINITION Sequence 73 from Patent WO0123605.
 ACCESSION AX105801
 VERSION AX105801.1 GI:13921814
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE
 AUTHORS Pandke,M., Gasch,A. and Berghof,K.
 TITLE Method and nucleic acids for determining the presence of
 JOURNAL micro-organisms specific to the brewing process
 PATENT: WO 0123605-A 73 05-APR-2001;
 Biotechon Diagnostics GmbH (DE)
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 Db 1 TCGAGATTAATGATTAATATCTAG 25

RESULT 2
 AX105729 267 bp DNA linear PAT 30-APR-2001
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 DEFINITION AX105729
 ACCESSION AX105729
 VERSION AX105729.1 GI:13921742
 KEYWORDS
 SOURCE Lactobacillus brevis
 ORGANISM Lactobacillus brevis
 Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 Lactobacillus.
 REFERENCE
 AUTHORS Pandke,M., Gasch,A. and Berghof,K.
 TITLE Method and nucleic acids for determining the presence of
 JOURNAL micro-organisms specific to the brewing process
 PATENT: WO 0123605-A 1 05-APR-2001;
 Biotechon Diagnostics GmbH (DE)
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 /mol_type="unassigned DNA"
 /db_xref="taxon:1580"

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 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 125 TCGAGATTAATGATTAATATCTAG 149

RESULT 3
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 LOCUS Homo sapiens chromosome 8 clone RP11-214U7 map 8, LOW-PASS SEQUENCE
 DEFINITION
 SAMPLING.
 ACCESSION AC079132
 VERSION AC079132.2 GI:13112249
 HTG: HTGS PHASEO.
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 REFERENCE
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 TITLE Homo sapiens chromosome 8, clone RP11-214U7
 JOURNAL Unpublished
 REFERENCE
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Barta,N., Bastien,V., Beda,F., Boguslavsky,L.,
 Boukhalter,B., Brown,A., Burkett,G., Campoliano,A., Castle,A.,
 Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P.,
 Dearliano,K., Dewar,K., Diaz,J.S., Dodg,S., Ferreira,P.,
 Fitzhugh,W., Gage,D., Galagan,J., Gardys,S., Ginde,S., Goyette,M.,
 Graham,L., Grand-Pierre,N., Hagos,B., Hesford,A., Horton,L.,
 Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Labèque,K.,
 Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lien,C., Liu,G.,
 MacDonald,P., Margulis,N., McCarthy,M., McEwan,P., McKernan,K.,
 McPheters,R., Meldrum,D., Menus,L., Mhova,T., Mienga,V.,
 Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
 O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K.,
 Pierre,N., Pisanl,C., Pollara,V., Raymond,C., Rieback,M., Riley,R.,
 Rogov,P., Rottman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
 Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,D., Testaye,S., Theodore,J.,
 Tirrell,A., Travers,M., Triggilo,J., Vassiliev,H., Viel,R., Vo,A.,
 Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
 Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (19-AUG-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Feb 23, 2001 this sequence version replaced gi:9857544.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

COMMENT
 JOURNAL
 TITLE
 JOURNAL

Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WISR
 Web site: http://www-seg.wi.mit.edu
 Contact: sequence submissions@genome.wi.mit.edu
 Project Information
 Center project name: L10419
 Center clone name: 214_U_7

* NOTE: This record contains 81 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

* 1 661: contig of 661 bp in length
 * 662 761: gap of 100 bp
 * 762 1473: contig of 712 bp in length

Tue Nov 16 16:09:52 2004

us-10-088-666-21.01g10.rst

Page 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-10-088-666-21

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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	17	81.0	797	7	CK096311 UB10CP810
5	16	76.2	228	9	CR349126 Medicago
6	16	76.2	544	9	CG467736 ZMMEB025
7	16	76.2	588	8	BZ294416 CG0884.F1
8	16	76.2	648	9	BZ294416 CG0884.F1
9	16	76.2	674	9	CG307773 ZMMEB051
10	16	76.2	682	5	CG307773 ZMMEB051
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12	16	76.2	702	8	BH179655 BH179655
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20	16	76.2	959	9	CG044756 PURSX79TB
21	16	76.2	985	9	CG009999 OGLU26TH
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23	16	76.2	1022	8	CG370241 PUBH44TB
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C	27	15	71.4	342	8	CC400403	CC400403
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C	30	15	71.4	420	9	CC719572	CC719572
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C	33	15	71.4	480	1	AU168090	AU168090
C	34	15	71.4	480	5	BP047360	BP047360
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C	42	15	71.4	535	4	BM347245	BM347245
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C	50	15	71.4	568	4	BU122973	BU122973
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C	52	15	71.4	574	8	CC345942	CC345942
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C	56	15	71.4	585	6	CB102412	CB102412
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C	69	15	71.4	712	8	BZ685709	BZ685709
C	70	15	71.4	721	6	CB102546	CB102546
C	71	15	71.4	743	9	AG446717	AG446717
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C	86	15	71.4	903	9	CG325319	CG325319
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CB102538	MWV_S0010
CC719572	OGWHPA8TH
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CK583556	ISR_W15_4
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AV767679	AV767679
BP040971	BP040971
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CK583669	ISR_W15_5
CK583445	ISR_W15_4
BM275391	PIESTOAC6
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AW734365	SK19C04.Y
CK583684	ISR_W15_5
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CB102087	MWV_S0002
BU122833	BU122833
BU122973	BU122973
AU200886	AU200886
CC345942	OGPAX22TV
CK583435	ISR_W15_4
CAB56682	PIESTOAC1
BU108163	BU108163
CB102412	MWV_S0008
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CB102156	MWV_S0004
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EM584859	17006594
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AV841373	ISR_W15_3
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BZ639321	OCCTB3TM
CK453913	911160_MA
CC035870	EST814254
CF812632	EST814254
CC436559	PHLL79TD
CC016802	EST787184
CO014788	EST787184
CG325319	OCG2C17TH
CF814429	EST691811
CO017225	EST787607
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CF818080	EST695462
CC0032335	EST810719
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AA259220	MAIMR043
BI863831	kx48n09.Y
AI093870	q3a0e08.S

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 BHS42735 14 66.7 288 1 AA791342
 C 100 14 66.7 328 7 COT50077 KBAE004P

ALIGNMENTS

RESULT 1
 BHS42735 779 bp DNA linear GSS 14-DEC-2001
 DEFINITION BOGXU95TR BOGX Brassica oleracea genomic clone BOGXU95, genomic
 survey sequence.

ACCESSION BHS42735
 VERSION BHS42735.1 GI:17794516
 KEYWORDS
 ORGANISM Brassica oleracea
 Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 779)
 Town, C.D., Van Aken, S., Uteerback, T., Koo, H. and Fraser, C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished (2001)
 Other GSSs: BOGXU95TR
 Contact: Chris Town

REFERENCE
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 JOURNAL
 COMMENT DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends.

FEATURES

Source
 1..779
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO1000DH3"
 /db_xref="taxon:3712"
 /clone="BOGXU95"
 /clone_1ib="BOGX"
 /note="Vector: pHD10, Site_1: BstXI; 2-3 kb sheared
 genomic DNA inserted into pHD10 using BstXI linkers"

ORIGIN

Query Match 85.7%; Score 18; DB 8; Length 779;
 Best Local Similarity 100.0%; Pred.No. 1.5;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGTCACACGCTAGT 19
 Db 356 CAAGTCACACGCTAGT 373

RESULT 2
 BU225601/c 727 bp mRNA linear EST 26-NOV-2002
 LOCUS BU225601 603401079F1 CSEQCHN23 Gallus gallus cDNA clone CSEST955n19 5', mRNA
 DEFINITION sequence.
 ACCESSION BU225601
 VERSION BU225601.1 GI:25461670
 KEYWORDS EST
 ORGANISM Gallus gallus (chicken)
 Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 727)
 Boardman, P.E., Sanz-Rzquero, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken CDVs

JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 2233534
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES

Source
 1..727
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hisex"
 /db_xref="taxon:9031"
 /clone="CSEST955n19"
 /dev_stage="22"
 /lab_host="DH10B"
 /clone_1ib="CSEQCHN23"
 /note="Organ: head; Vector: pBluescript II KS(+); Site_1:
 EcoRI; Site_2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this, first strand reaction, double-stranded cDNA
 was bluntended, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldi et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN

Query Match 81.0%; Score 17; DB 5; Length 727;
 Best Local Similarity 100.0%; Pred.No. 6;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAAGTCACACGCTAG 17
 Db 91 CCAAGTCACACGCTAG 75

RESULT 3
 CG361559 796 bp DNA linear GSS 26-AUG-2003
 LOCUS CG361559 CG1DP94TH ZM 0.7 1.5 KB Zea mays genomic clone ZMMEM40739020,
 DEFINITION genomic survey sequence.
 ACCESSION CG361559
 VERSION CG361559.1 GI:34278826
 KEYWORDS GSS.
 ORGANISM Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 796)
 White, C.A., Quackenbush, J., Van Aken, S., Uteerback, T.,
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, V.A., Kohlring, T.,
 Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
 Consortium for Maize Genomics
 Unpublished (2002)
 Other GSSs: CG1DP94TV
 Contact: Cathy White

REFERENCE
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: white@tigr.org
 Seq primer: TR

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:59:59 ; Search time 48.4234 Seconds
(without alignments)
2710.166 Million cell updates/sec

Title: US-10-088-666-73

Perfect score: 25

Sequence: 1 tcgagataatgataatatactag 25

Scoring table: **OLIGO-NUC**
Gapop 60.0, Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size: 10

Total number of hits satisfying chosen parameters: 72573

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : N_Geneseq_23Sep04:*
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2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002as:*
7: Geneseq2002bs:*
8: Geneseq2003as:*
9: Geneseq2003bs:*
10: Geneseq2003cs:*
11: Geneseq2003ds:*
12: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	5	AA61638 Lactobaci
2	25	100.0	267	5	AA61666 Lactobaci
3	18	72.0	1190	2	AA113651 Enterococ
4	18	72.0	1190	6	AB899446 Enterococ
5	18	72.0	5962	6	AB133286 Human imm
6	17	68.0	672	8	ACA43195 Prokaryot
7	17	68.0	177531	8	ACR62732 Cancer ba
8	17	68.0	177531	8	AD20847 MRP1 base
9	17	68.0	177531	10	ADB87936 Human UGT
10	17	68.0	177531	10	ADB96919 Human MDR
11	17	68.0	177531	10	ADH92110 Human MDR
12	17	68.0	177531	10	ADH74617 Human BAC
13	17	68.0	195917	12	AD20606 Human sof
14	16	64.0	358	5	ABV34455 Human pro
15	16	64.0	395	6	ABN21213 Human ORF
16	16	64.0	455	4	ABA26661 Probe #51
17	16	64.0	497	5	ABV13034 Human pro
18	16	64.0	1506	10	ACF71932 Photorhab
19	16	64.0	2136	8	ACA33620 Prokaryot
20	16	64.0	2415	8	ACA43403 Prokaryot
21	16	64.0	2426	6	ABQ76758 Human gon

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c 23	16	64.0	6527	2	AA60141 Antirrhin
c 24	16	64.0	8979	6	ABL32785 Human imm
c 25	16	64.0	8979	6	ABK31271 Signal tr
c 26	16	64.0	8979	6	ABL70232 Chemical
c 27	16	64.0	8979	6	AA61179 Human gen
c 28	16	64.0	25426	8	ADA41645 Human sec
c 29	16	64.0	25426	8	ACC50940 Human sec
c 30	16	64.0	25426	10	ADD38155 CDNA clon
c 31	16	64.0	25426	10	ADA57777 BAC fragm
c 32	16	64.0	110000	10	ACR67367 51
c 33	16	64.0	110000	10	ACF65387-2
c 34	16	64.0	322101	10	AA58431 Human PFO
c 35	16	64.0	322101	12	AD135046 Human pro
c 36	15	60.0	150	6	ABN16840 Human ORF
c 37	15	60.0	326	8	ABX51125 Bovine ES
c 38	15	60.0	480	6	ABT10253 Human bre
c 39	15	60.0	525	10	ADD16647 DNA (Seq1
c 40	15	60.0	529	4	AAK6957 Human imm
c 41	15	60.0	529	4	AAK6957 Human CDN
c 42	15	60.0	535	12	ACH71148 Human sec
c 43	15	60.0	572	3	AA87766 Human sec
c 44	15	60.0	572	5	AA64048 Human sec
c 45	15	60.0	572	12	ADP18786 Human sec
c 46	15	60.0	593	5	ABV55376 Human pro
c 47	15	60.0	703	2	AAZ15924 Human gen
c 48	15	60.0	766	4	AAH34697 Human col
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c 51	15	60.0	854	12	ADP19107 Human sec
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c 55	15	60.0	1901	4	AAH17036 Human CDN
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c 57	15	60.0	2136	4	AA162899 Human gen
c 58	15	60.0	2581	10	ADFR9810 Triteipen
c 59	15	60.0	2988	2	AAZ02289 Borrelia
c 60	15	60.0	3001	3	AAH51775 Chromosom
c 61	15	60.0	3193	4	ABL04126 Drosophi1
c 62	15	60.0	3380	4	ABL16198 Drosophi1
c 63	15	60.0	3519	8	ACA33811 Prokaryot
c 64	15	60.0	3552	10	ADC93399 E. faeciu
c 65	15	60.0	3937	10	ADRS3913 Human pro
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c 78	15	60.0	11021	4	ABL11102 Drosophi1
c 79	15	60.0	11157	6	ABL132605 Human imm
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c 82	15	60.0	18624	6	ABL133703 Human imm
c 83	15	60.0	22875	4	ABL128654 Drosophi1
c 84	15	60.0	24389	4	ABL199006 Drosophi1
c 85	15	60.0	33472	4	ABL19792 Drosophi1
c 86	15	60.0	48000	9	AAFP7996 Human cal
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c 89	15	60.0	68233	11	ADA66349 Mouse PpP
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c 92	15	60.0	110000	6	ABA50521_19
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Ab132785 Human imm
Ab131271 Signal tr
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Acc50940 Human sec
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Aa162903 Human gen
Aah17036 Human CDN
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Aa162899 Human gen
Adfr9810 Triteipen
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Aah51775 Chromosom
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Ab134142 Human imm
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Ab132605 Human imm
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Ab133703 Human imm
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Continuation (2 of

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98	15	60.0	177851	8	AA157272	AA157272 BA438B23-
99	15	60.0	266145	10	AD87477	AD87477 Fowlpox v
100	15	60.0	340449	8	AA152198	AA152198 Human sec

ALIGNMENTS

RESULT 1

AA161370 standard; DNA; 25 BP.

ID AAF61638

AC AAF61638;

DT 02-JUL-2001 (first entry)

DE Lactobacillus brevis 23S rRNA/5S rRNA specific probe SEQ ID 73.

KM 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.

XX Lactobacillus brevis.

XX DE19945964-A1.

XX PD 05-APR-2001.

XX PF 24-SEP-1999; 99DE-01045964.

XX PR 24-SEP-1999; 99DE-01045964.

XX PA (BIOT-) BIOTECON DIAGNOSTICS GMBH.

XX PI Fandke M, Gasch A, Berghof K;

XX DR WPI; 2001-246136/26.

PT Detecting contaminating microorganisms in brewing, by nucleic acid
 PT amplification and hybridization, either non-specific or genus- or species
 PT specific.

XX PS Claim 9(1); Page 17; 48pp; German.

XX This invention describes a novel method for detecting microorganisms (A)
 CC of importance in brewing which comprises treating a sample with at least
 CC two primers (P1) that hybridize to a consensus region in the nucleic acid
 CC of (A), at least part of the microbial nucleic acid is amplified, the
 CC amplicon is treated with at least one probe (P2) that hybridizes
 CC specifically with a sequence common to all (A) or specific for one or
 CC more families, genera or species, and any formation of hybrids is
 CC detected. The method is used to detect, identify and/or characterize
 CC microorganisms in beer or brewing materials, particularly for detecting
 CC contamination. The method may detect the entire range of contaminating
 CC microbes, either as a general test for contamination or as a test
 CC specific for particular genera or (sub)species. It is quicker than known
 CC microbiological methods, and can detect several organisms in the same
 CC sample, including organisms not presently recognized as contaminants. The
 CC method provides an early indication of contamination and can be automated
 CC for high throughput analysis

SQ Sequence 25 BP; 11 A; 2 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 5; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.0015;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGAGATATATGATATATCTAG 25

Db 1 TCGAGATATATGATATATCTAG 25

AA161566	267	BP.
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ID AAF61566

AC AAF61566;

DT 02-JUL-2001 (first entry)

DE Lactobacillus brevis 23S rRNA-spacer-5S rRNA DNA fragment.

KM 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.

XX Lactobacillus brevis.

XX DE19945964-A1.

XX PD 05-APR-2001.

XX PF 24-SEP-1999; 99DE-01045964.

XX PR 24-SEP-1999; 99DE-01045964.

XX PA (BIOT-) BIOTECON DIAGNOSTICS GMBH.

XX PI Fandke M, Gasch A, Berghof K;

XX DR WPI; 2001-246136/26.

PT Detecting contaminating microorganisms in brewing, by nucleic acid
 PT amplification and hybridization, either non-specific or genus- or species
 PT specific.

XX PS Claim 9(1); Page 9; 48pp; German.

XX This invention describes a novel method for detecting microorganisms (A)
 CC of importance in brewing which comprises treating a sample with at least
 CC two primers (P1) that hybridize to a consensus region in the nucleic acid
 CC of (A), at least part of the microbial nucleic acid is amplified, the
 CC amplicon is treated with at least one probe (P2) that hybridizes
 CC specifically with a sequence common to all (A) or specific for one or
 CC more families, genera or species, and any formation of hybrids is
 CC detected. The method is used to detect, identify and/or characterize
 CC microorganisms in beer or brewing materials, particularly for detecting
 CC contamination. The method may detect the entire range of contaminating
 CC microbes, either as a general test for contamination or as a test
 CC specific for particular genera or (sub)species. It is quicker than known
 CC microbiological methods, and can detect several organisms in the same
 CC sample, including organisms not presently recognized as contaminants. The
 CC method provides an early indication of contamination and can be automated
 CC for high throughput analysis

SQ Sequence 267 BP; 77 A; 51 C; 77 G; 62 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 5; Length 267;

Best Local Similarity 100.0%; Pred. No. 0.0012;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGAGATATATGATATATCTAG 25

Db 125 TCGAGATATATGATATATCTAG 149

RESULT 3

AA13651/c

ID AAX13651 standard; DNA; 1190 BP.

AC AAX13651;

DT 19-MAR-1999 (first entry)

DE Enterococcus faecalis genome contig SEQ ID NO:714.

KM Enterococcus faecalis; contig; detection; Enterococcal infection;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:28:49 ; Search time 36.1351 Seconds
(without alignments)
3138.794 Million cell updates/sec

Title: US-10-088-666-21

Perfect score: 21 ccaagtcacacacgtagtctg 21

Scoring table: OLIGO_NUC;
Gapop 60.0 , Gapext 60.0

Searched: 3625171 seqs, 2700493622 residues

Word size: 10

Total number of hits satisfying chosen parameters: 28758

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Listing first 100 summaries

Database : Published Applications NA:*

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18:	/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
19:	/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	76.2	365	16	US-10-424-599-100843
2	15	71.4	395	16	US-10-424-599-97864
3	15	71.4	621	17	US-10-767-795-4222
4	15	71.4	741	15	US-10-369-493-30596
5	15	71.4	1134	16	US-10-425-114-20775
6	15	71.4	1134	18	US-10-425-115-16878
7	15	71.4	1156	16	US-10-425-114-10548
8	15	71.4	1161	16	US-10-424-599-99681
9	15	71.4	1188	16	US-10-424-599-133586
10	15	71.4	168276	13	US-10-087-192-142
11	14	66.7	254	17	US-10-437-963-8513
12	14	66.7	559	13	US-10-027-632-241832

C 13	14	66.7	559	15	US-10-027-632-241832	Sequence 241832, A
C 14	14	66.7	561	17	US-10-437-963-32347	Sequence 32347, A
C 15	14	66.7	591	13	US-10-029-386-7736	Sequence 7736, Ap
C 16	14	66.7	601	13	US-10-027-632-199748	Sequence 199748, A
C 17	14	66.7	601	13	US-10-027-632-199749	Sequence 199749, A
C 18	14	66.7	601	15	US-10-027-632-199748	Sequence 199748, A
C 19	14	66.7	601	15	US-10-027-632-199749	Sequence 199749, A
C 20	14	66.7	1203	13	US-10-027-632-199747	Sequence 199747, A
C 21	14	66.7	1203	15	US-10-027-632-199747	Sequence 199747, A
C 22	14	66.7	1613	17	US-10-451-467A-259	Sequence 259, App
C 23	14	66.7	1650	16	US-10-282-122A-30915	Sequence 30915, A
C 24	14	66.7	1820	17	US-10-437-963-97628	Sequence 97628, A
C 25	14	66.7	2000	16	US-10-260-238-1734	Sequence 1734, Ap
C 26	14	66.7	2347	16	US-10-424-599-54300	Sequence 54300, A
C 27	14	66.7	2732	15	US-10-369-493-36202	Sequence 36202, A
C 28	14	66.7	2796	17	US-10-437-963-97626	Sequence 97626, A
C 29	14	66.7	3825	9	US-09-746-491-11	Sequence 11, App1
C 30	14	66.7	19639	8	US-08-910-386A-6	Sequence 6, App1
C 31	14	66.7	143973	13	US-10-087-192-442	Sequence 442, App
C 32	13	61.9	25	15	US-10-098-263B-47079	Sequence 47079, A
C 33	13	61.9	180	17	US-10-767-701-23303	Sequence 23203, A
C 34	13	61.9	207	9	US-09-960-352-4229	Sequence 4229, Ap
C 35	13	61.9	211	9	US-09-960-352-2061	Sequence 2061, Ap
C 36	13	61.9	229	9	US-09-960-352-4220	Sequence 4220, Ap
C 37	13	61.9	239	9	US-09-960-352-13451	Sequence 13451, A
C 38	13	61.9	242	9	US-09-960-352-2998	Sequence 2998, Ap
C 39	13	61.9	247	9	US-09-960-352-183	Sequence 183, App
C 40	13	61.9	281	9	US-09-960-352-9850	Sequence 9850, Ap
C 41	13	61.9	302	9	US-09-960-352-7737	Sequence 7737, Ap
C 42	13	61.9	301	9	US-09-960-352-86	Sequence 86, App1
C 43	13	61.9	308	9	US-09-960-352-10392	Sequence 10392, A
C 44	13	61.9	310	16	US-10-424-599-104720	Sequence 104720, A
C 45	13	61.9	324	10	US-09-764-891-692	Sequence 692, App
C 46	13	61.9	325	17	US-10-091-572-56	Sequence 56, App1
C 47	13	61.9	325	14	US-10-437-963-33253	Sequence 33253, A
C 48	13	61.9	337	10	US-09-764-891-6697	Sequence 6697, Ap
C 49	13	61.9	337	10	US-09-764-891-6698	Sequence 6698, Ap
C 50	13	61.9	337	14	US-10-091-572-558	Sequence 558, App
C 51	13	61.9	337	14	US-10-091-572-559	Sequence 559, App
C 52	13	61.9	340	9	US-09-960-352-2761	Sequence 2761, Ap
C 53	13	61.9	341	9	US-09-960-352-2191	Sequence 2191, Ap
C 54	13	61.9	341	16	US-10-424-599-12628	Sequence 12628, A
C 55	13	61.9	348	9	US-09-960-352-11402	Sequence 11402, A
C 56	13	61.9	358	9	US-09-960-352-9403	Sequence 9403, Ap
C 57	13	61.9	358	9	US-09-960-352-8472	Sequence 8472, Ap
C 58	13	61.9	360	9	US-09-960-352-2079	Sequence 2079, Ap
C 59	13	61.9	360	9	US-09-960-352-12857	Sequence 12857, A
C 60	13	61.9	366	9	US-09-960-352-8659	Sequence 8659, Ap
C 61	13	61.9	366	9	US-09-960-352-14094	Sequence 14094, A
C 62	13	61.9	368	9	US-09-960-352-4223	Sequence 4223, Ap
C 63	13	61.9	378	9	US-09-960-352-2966	Sequence 2966, Ap
C 64	13	61.9	384	9	US-09-960-352-215	Sequence 215, App
C 65	13	61.9	384	17	US-10-767-701-30666	Sequence 30666, A
C 66	13	61.9	385	9	US-09-960-352-10641	Sequence 10641, A
C 67	13	61.9	387	9	US-09-960-352-13175	Sequence 13175, A
C 68	13	61.9	391	9	US-09-783-590-9798	Sequence 9798, Ap
C 69	13	61.9	391	9	US-09-960-352-10595	Sequence 10595, A
C 70	13	61.9	395	9	US-09-960-352-2505	Sequence 2505, Ap
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C 72	13	61.9	399	9	US-09-960-352-9396	Sequence 9396, Ap
C 73	13	61.9	404	9	US-09-960-352-179	Sequence 179, App
C 74	13	61.9	404	9	US-09-960-352-2789	Sequence 2789, Ap
C 75	13	61.9	404	9	US-09-960-352-7246	Sequence 7246, Ap
C 76	13	61.9	405	10	US-09-803-719-766	Sequence 766, App
C 77	13	61.9	405	16	US-10-424-599-45029	Sequence 45029, A
C 78	13	61.9	405	9	US-09-960-352-12380	Sequence 12380, A
C 79	13	61.9	406	9	US-09-960-352-9848	Sequence 9848, Ap
C 80	13	61.9	407	9	US-09-960-352-11517	Sequence 11517, A
C 81	13	61.9	416	9	US-09-960-352-10053	Sequence 10053, A
C 82	13	61.9	417	16	US-10-424-599-124751	Sequence 124751, A
C 83	13	61.9	419	9	US-09-960-352-7509	Sequence 7509, App
C 84	13	61.9	420	9	US-09-960-352-6117	Sequence 6117, Ap

86 13 61.9 427 9 US-09-960-352-7803 Sequence 7803, Ap
87 13 61.9 430 9 US-09-960-352-5911 Sequence 5911, Ap
88 13 61.9 441 17 US-10-437-963-25328 Sequence 25328, A
89 13 61.9 458 17 US-09-960-352-9145 Sequence 9145, Ap
90 13 61.9 468 17 US-10-437-963-18379 Sequence 18379, A
91 13 61.9 496 15 US-10-027-632-126514 Sequence 126514, A
92 13 61.9 496 15 US-10-027-632-126514 Sequence 126514, A
93 13 61.9 499 9 US-09-864-761-10086 Sequence 10086, A
94 13 61.9 505 13 US-10-027-632-199383 Sequence 199383, A
95 13 61.9 508 15 US-10-027-632-199383 Sequence 199383, A
96 13 61.9 505 16 US-10-424-599-18750 Sequence 18750, A
97 13 61.9 517 16 US-10-424-599-24383 Sequence 24383, A
98 13 61.9 526 16 US-10-424-599-41897 Sequence 41897, A
99 13 61.9 535 9 US-09-867-550-1313 Sequence 1313, Ap
100 13 61.9 542 13 US-10-027-632-50508 Sequence 50508, A

ALIGNMENTS

RESULT 1
US-10-424-599-100843
; Sequence 100843, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 100843
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_62074C.1
US-10-424-599-100843

Query Match 76.2%; Score 16; DB 16; Length 365;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGTCAACAAGTACTT 19
DB 124 AGTCAACAAGTACTT 139

RESULT 2
US-10-424-599-97864/C
; Sequence 97864, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 97864
; LENGTH: 395
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59385C.1

US-10-424-599-97864
Query Match 71.4%; Score 15; DB 16; Length 395;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTCAACAAGTACTT 19
DB 125 GTCAACAAGTACTT 111

RESULT 3
US-10-767-795-4222/C
; Sequence 4222, Application US/10767795
; Publication No. US2004018130A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53534) B
; CURRENT APPLICATION NUMBER: US/10/767,795
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 117596
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; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C111_9
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Best Local Similarity 100.0%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 30596, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052) B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
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; LENGTH: 741
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-10-369-493-30596

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAAGTCAACAAGCT 15
DB 88 CCAAGTCAACAAGCT 102

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:18:54 ; Search time 8.95496 Seconds
(without alignments)
1666.850 Million cell updates/sec

Title: US-10-088-666-21

Perfect score: 21

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Scoring table: OLIGO-NUC

Gapop 60.0, Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size: 10

Total number of hits satisfying chosen parameters: 4843

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

Issued Patents NA:
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6: /cgn2_6/prodata/1/ina/backfltest.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	66.7	610	4	US-09-270-767-12339
2	13	61.9	186	4	US-09-248-796A-74368
3	13	61.9	189	4	US-09-583-110-2597
4	13	61.9	360	4	US-09-134-000C-796
5	13	61.9	396	4	US-09-252-991A-6239
6	13	61.9	525	4	US-09-248-796A-1527
7	13	61.9	564	4	US-09-583-110-2598
8	13	61.9	639	4	US-09-248-796A-6195
9	13	61.9	708	1	US-07-794-398B-1
10	13	61.9	708	1	US-08-002-866-1
11	13	61.9	780	4	US-09-248-796A-6461
12	13	61.9	954	4	US-09-248-796A-2947
13	13	61.9	963	4	US-09-328-352-3811
14	13	61.9	997	4	US-09-690-454-33
15	13	61.9	1089	4	US-09-291-299A-5
16	13	61.9	1101	4	US-09-248-796A-1389
17	13	61.9	1236	4	US-09-016-434-717
18	13	61.9	1243	1	US-08-702-344-27
19	13	61.9	1266	4	US-09-248-796A-314
20	13	61.9	1272	4	US-09-489-039A-5398
21	13	61.9	1295	4	US-09-219-194-3
22	13	61.9	1399	4	US-09-248-796A-5857
23	13	61.9	1392	4	US-09-270-767-10521
24	13	61.9	1311	4	US-09-248-796A-5537
25	13	61.9	1317	4	US-09-248-796A-5750
26	13	61.9	1318	4	US-09-270-767-29088
27	13	61.9	1356	4	US-09-489-039A-5355

28	13	61.9	1413	4	US-09-134-000C-2063
29	13	61.9	1505	4	US-08-221-299A-2
30	13	61.9	1523	4	US-09-291-299A-4
31	13	61.9	1950	4	US-09-270-767-13177
32	13	61.9	2073	4	US-09-248-796A-5066
33	13	61.9	2130	4	US-09-583-110-2452
34	13	61.9	2133	4	US-09-248-796A-302
35	13	61.9	2218	2	US-08-421-044-1
36	13	61.9	2307	4	US-08-792-924-43
37	13	61.9	2342	1	US-08-441-170-1
38	13	61.9	2669	1	US-08-118-101A-3
39	13	61.9	2670	4	US-09-614-221A-540
40	13	61.9	4565	3	US-08-776-265-2
41	13	61.9	4565	4	US-09-398-184-2
42	13	61.9	5240	4	US-09-171-337A-2
43	13	61.9	5240	4	US-09-611-022-2
44	13	61.9	8791	5	PCT-US96-01735-5
45	13	61.9	9610	4	US-09-566-921-45
46	13	61.9	9848	4	US-09-385-222A-3
47	13	61.9	15363	4	US-08-961-527-139
48	12	57.1	85	3	US-07-729-513-9
49	12	57.1	85	3	US-09-364-543-57
50	12	57.1	90	3	US-08-974-549A-685
51	12	57.1	90	3	US-08-974-549A-686
52	12	57.1	90	4	US-09-721-456-685
53	12	57.1	90	4	US-09-721-456-686
54	12	57.1	108	5	PCT-US95-09589-6
55	12	57.1	108	5	PCT-US95-09589A-6
56	12	57.1	227	4	US-09-513-899C-30518
57	12	57.1	267	4	US-09-252-911A-6214
58	12	57.1	286	4	US-09-270-767-14783
59	12	57.1	291	4	US-09-313-294A-6338
60	12	57.1	324	4	US-09-270-767-10980
61	12	57.1	330	5	PCT-US95-09589-1
62	12	57.1	330	5	PCT-US95-09589A-1
63	12	57.1	350	2	US-08-967-101-35
64	12	57.1	350	2	US-08-952-541-35
65	12	57.1	350	3	US-09-124-698-35
66	12	57.1	350	3	US-09-127-480-35
67	12	57.1	350	3	US-08-496-841C-35
68	12	57.1	350	3	US-09-124-523-35
69	12	57.1	350	4	US-09-636-796A-35
70	12	57.1	350	4	US-08-431-048E-35
71	12	57.1	358	4	US-09-016-434-707
72	12	57.1	372	4	US-09-134-000C-13674
73	12	57.1	400	4	US-08-781-986A-3674
74	12	57.1	422	4	US-09-248-796A-3904
75	12	57.1	444	4	US-09-248-796A-8988
76	12	57.1	444	4	US-09-221-017B-119
77	12	57.1	457	4	US-09-270-767-10199
78	12	57.1	457	4	US-09-513-999E-4086
79	12	57.1	461	4	US-09-270-767-10077
80	12	57.1	462	4	US-09-187-999-32
81	12	57.1	551	4	US-09-370-767-26085
82	12	57.1	555	4	US-09-543-681A-2575
83	12	57.1	564	3	US-08-598-816-159
84	12	57.1	570	3	US-09-325-932A-6
85	12	57.1	600	4	US-09-248-796A-3523
86	12	57.1	615	4	US-09-448-796A-5523
87	12	57.1	618	4	US-09-443-681A-3028
88	12	57.1	624	3	US-09-415-522-1
89	12	57.1	636	4	US-09-669-951-12
90	12	57.1	665	4	US-09-352-991A-6331
91	12	57.1	668	4	US-08-956-711E-3658
92	12	57.1	668	4	US-08-781-986A-3658
93	12	57.1	735	4	US-09-328-352-1471
94	12	57.1	749	4	US-09-270-767-13258
95	12	57.1	778	4	US-09-325-932A-7
96	12	57.1	783	4	US-09-352-991A-6415
97	12	57.1	819	2	US-08-441-157-3
98	12	57.1	819	3	US-08-642-807A-31
99	12	57.1	819	3	US-08-193-159-3
100	12	57.1	819	4	US-09-252-991A-6136

ALIGNMENTS

RESULT 1

US-09-270-767-12339
; Sequence 12339, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12339
; LENGTH: 610
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-12339

Query Match 66.7%; Score 14; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 16;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTCACACAGCTAGT 18
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DB 498 GTCACACAGCTAGT 511

RESULT 2

US-09-248-796A-7468
; Sequence 7468, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 7468
; LENGTH: 186
; TYPE: DNA
; ORGANISM: *Candida albicans*
US-09-248-796A-7468

Query Match 61.9%; Score 13; DB 4; Length 186;
Best Local Similarity 100.0%; Pred. No. 61;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAAGTCACACAC 13
|||||

DB 4 CCAAGTCACACAC 16

RESULT 3

US-09-583-110-2597/C
; Sequence 2597, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to *Streptococcus*
; FILE REFERENCE: PAT000-07A
; CURRENT APPLICATION NUMBER: US/09/583,110

; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 2597
; LENGTH: 189
; TYPE: DNA
; ORGANISM: *Streptococcus pneumoniae*
US-09-583-110-2597

Query Match 61.9%; Score 13; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 61;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAAGTCACACAC 13
|||||

DB 174 CCAAGTCACACAC 162

RESULT 4

US-09-134-000C-796/C
; Sequence 796, Application US/09134000C
; Patent No. 6617136
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 796
; LENGTH: 360
; TYPE: DNA
; ORGANISM: *Enterococcus faecalis*
US-09-134-000C-796

Query Match 61.9%; Score 13; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 62;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAAGTCACACAC 13
|||||

DB 265 CCAAGTCACACAC 253

RESULT 5

US-09-252-991A-6239
; Sequence 6239, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PSEUDOMONAS*
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6239
; LENGTH: 396
; TYPE: DNA
; ORGANISM: *Pseudomonas aeruginosa*

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:59:59 ; Search time 40.6757 Seconds
(without alignments)
2710.166 Million cell updates/sec

Title: US-10-088-666-21

Perfect score: 21
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Searched: 4134886 seqs, 2624710521 residues

Word size: 10

Total number of hits satisfying chosen parameters: 31333

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

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1: geneseqn1980s:*
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11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	5	AaF61586
2	21	100.0	267	5	AaF61566
3	18	85.7	2215	3	AaA43884
4	14	66.7	546	6	ABN23311
5	14	66.7	591	12	ACH74541
6	14	66.7	668	3	AFI13909
7	14	66.7	729	6	AB862906
8	14	66.7	729	6	ABF11511
9	14	66.7	750	11	ADM45774
10	14	66.7	766	6	AB862991
11	14	66.7	766	6	ABF11596
12	14	66.7	789	10	ADM45602
13	14	66.7	789	11	ADM45503
14	14	66.7	812	6	AB863068
15	14	66.7	813	6	ABF11673
16	14	66.7	935	10	ADOC72635
17	14	66.7	935	10	ADOC72635
18	14	66.7	1613	6	ABO76417
19	14	66.7	1650	4	ACA43045
20	14	66.7	1680	4	ABF21577
21	14	66.7	2000	12	ADJ40734

22	14	66.7	3070	10	ADP47979	Ad47979 Human gen
23	14	66.7	3591	12	ADN13951	Adn13951 Human pro
24	14	66.7	3825	4	AAC86158	Aac86158 FCIR6 nuc
25	14	66.7	4141	4	ABL21576	AbL21576 Drosophila
26	14	66.7	19639	2	AAX23524	Aax23524 O. longis
27	14	66.7	110000	12	ADN46845_10	ADN46845_10
28	14	66.7	110000	14	ADN47591_10	ADN47591_10
29	14	66.7	110000	12	ADN46123_10	ADN46123_10
30	14	66.7	110000	12	ADN47209_10	ADN47209_10
31	14	66.7	110000	12	ADN46464_10	ADN46464_10
32	14	66.7	110000	12	ADN47960_10	ADN47960_10
33	13	61.9	25	9	ACT47088	Act47088 Human mic
34	13	61.9	102	6	ABN71387	Abn71387 Streptococ
35	13	61.9	121	12	ADK33359	Adk33359 Polynucle
36	13	61.9	207	8	ABX39064	Abx39064 Bovine ES
37	13	61.9	211	8	ABX36896	Abx36896 Bovine ES
38	13	61.9	229	8	ABX38055	Abx38055 Bovine ES
39	13	61.9	239	8	ABX46286	Abx46286 Bovine ES
40	13	61.9	242	8	ABX37833	Abx37833 Bovine ES
41	13	61.9	244	6	AB862927	AB862927 Selected
42	13	61.9	247	8	ABT11532	ABT11532 Yeast sel
43	13	61.9	248	5	ABX35018	ABX35018 Bovine ES
44	13	61.9	248	5	AAI69939	AAI69939 Probe m19
45	13	61.9	281	8	ABX44685	ABX44685 Bovine ES
46	13	61.9	292	8	ABX42572	ABX42572 Bovine ES
47	13	61.9	301	8	ABX34921	ABX34921 Bovine ES
48	13	61.9	308	8	ABX45227	ABX45227 Bovine ES
49	13	61.9	324	4	AAI00691	AAI00691 Human rep
50	13	61.9	324	5	AA540115	AA540115 DNA encod
51	13	61.9	337	4	AAI04009	AAI04009 Human rep
52	13	61.9	337	4	AAI04010	AAI04010 Human rep
53	13	61.9	337	5	AA540406	AA540406 DNA encod
54	13	61.9	337	5	AA540407	AA540407 DNA encod
55	13	61.9	340	8	ABX37596	ABX37596 Bovine ES
56	13	61.9	341	8	ABX37026	ABX37026 Bovine ES
57	13	61.9	342	8	ABX46317	ABX46317 Bovine ES
58	13	61.9	345	10	ADK59305	Adk59305 Plant DNA
59	13	61.9	348	8	ABX44238	ABX44238 Bovine ES
60	13	61.9	352	3	AAH30860	AAH30860 Human col
61	13	61.9	358	8	ABX43307	ABX43307 Bovine ES
62	13	61.9	359	3	AAA43856	AAA43856 Human sec
63	13	61.9	360	8	ABX36914	ABX36914 Bovine ES
64	13	61.9	360	8	ABX47692	ABX47692 Bovine ES
65	13	61.9	360	10	ADH82911	Adh82911 Enterococ
66	13	61.9	363	5	ADM19610	Adm19610 Novel hum
67	13	61.9	366	8	ABX43494	ABX43494 Bovine ES
68	13	61.9	366	8	ABX48929	ABX48929 Bovine ES
69	13	61.9	368	8	ABX39058	ABX39058 Bovine ES
70	13	61.9	378	8	ABX37801	ABX37801 Bovine ES
71	13	61.9	382	8	ABX35050	ABX35050 Bovine ES
72	13	61.9	385	8	ABX45476	ABX45476 Bovine ES
73	13	61.9	387	8	ABX48010	ABX48010 Bovine ES
74	13	61.9	391	8	ABX45430	ABX45430 Bovine ES
75	13	61.9	395	8	ABX37340	ABX37340 Bovine ES
76	13	61.9	396	11	ABD07635	ABD07635 Pseudom
77	13	61.9	398	1	AAK62170	Aak62170 Human imm
78	13	61.9	398	8	ABX41848	ABX41848 Bovine ES
79	13	61.9	399	8	ABX44231	ABX44231 Bovine ES
80	13	61.9	404	8	ABX44724	ABX44724 Bovine ES
81	13	61.9	404	8	ABX35014	ABX35014 Bovine ES
82	13	61.9	404	8	ABX37630	ABX37630 Bovine ES
83	13	61.9	405	3	AA51811	AA51811 Arabidops
84	13	61.9	405	4	AA537708	AA537708 Novel hum
85	13	61.9	405	8	ABX42081	ABX42081 Bovine ES
86	13	61.9	406	8	ABX47215	ABX47215 Bovine ES
87	13	61.9	407	8	ABX44681	ABX44681 Bovine ES
88	13	61.9	408	3	AA51795	AA51795 Arabidops
89	13	61.9	416	8	ABX46352	ABX46352 Bovine ES
90	13	61.9	417	8	ABX44888	ABX44888 Bovine ES
91	13	61.9	419	8	ABX42344	ABX42344 Bovine ES
92	13	61.9	420	8	ABX40952	ABX40952 Bovine ES
93	13	61.9	427	8	ABX42638	ABX42638 Bovine ES
94	13	61.9	430	8	ABX40746	ABX40746 Bovine ES

95	13	61.9	444	6	ABN68526	Abn68526 Streptococcus
96	13	61.9	455	9	AC117009	AC117009 DNA clone
97	13	61.9	456	8	AB252858	AB252858 Aspergillus
98	13	61.9	458	8	ABX43980	ABX43980 Bovine ES
99	13	61.9	489	10	ADG37805	ADG37805 Aspergillus
100	13	61.9	499	4	AA133114	AA133114 Probe #18

ALIGNMENTS

RESULT 1

AAAF61586 standard; DNA; 21 BP.

AAAF61586;

02-JUL-2001 (first entry)

Lactobacillus brevis 23S rRNA/5S rRNA specific DNA probe.

23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.

Lactobacillus brevis.

DE19945964-A1.

05-APR-2001.

24-SEP-1999; 99DE-01045964.

24-SEP-1999; 99DE-01045964.

(BIOT-) BIOTECON DIAGNOSTICS GMBH.

Fandke M, Gasch A, Berghof K;

WPI; 2001-246136/26.

Detecting contaminating microorganisms in brewing, by nucleic acid

amplification and hybridization, either non-specific or genus- or species

specific.

Claim 9(1); Page 15; 48pp; German.

This invention describes a novel method for detecting microorganisms (A)

of importance in brewing which comprises treating a sample with at least

two primers (P1) that hybridize to a consensus region in the nucleic acid

of (A), at least part of the microbial nucleic acid is amplified, the

amplicon is treated with at least one probe (P2) that hybridizes

specifically with a sequence common to all (A) or specific for one or

more families, genera or species, and any formation of hybrids is

detected. The method is used to detect, identify and/or characterize

microorganisms in beer or brewing materials, particularly for detecting

contamination. The method may detect the entire range of contaminating

microbes, either as a general test for contamination or as a test

specific for particular genera or (sub) species. It is quicker than known

microbiological methods, and can detect several organisms in the same

sample, including organisms not presently recognized as contaminants. The

method provides an early indication of contamination and can be automated

for high throughput analysis

Sequence 21 BP; 7 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

95	13	61.9	444	6	ABN68526	Abn68526 Streptococcus
96	13	61.9	455	9	AC117009	AC117009 DNA clone
97	13	61.9	456	8	AB252858	AB252858 Aspergillus
98	13	61.9	458	8	ABX43980	ABX43980 Bovine ES
99	13	61.9	489	10	ADG37805	ADG37805 Aspergillus
100	13	61.9	499	4	AA133114	AA133114 Probe #18

ALIGNMENTS

RESULT 2

AAAF61566 standard; DNA; 267 BP.

AAAF61566;

02-JUL-2001 (first entry)

Lactobacillus brevis 23S rRNA-spacer-5S rRNA DNA fragment.

23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.

Lactobacillus brevis.

DE19945964-A1.

05-APR-2001.

24-SEP-1999; 99DE-01045964.

24-SEP-1999; 99DE-01045964.

(BIOT-) BIOTECON DIAGNOSTICS GMBH.

Fandke M, Gasch A, Berghof K;

WPI; 2001-246136/26.

Detecting contaminating microorganisms in brewing, by nucleic acid

amplification and hybridization, either non-specific or genus- or species

specific.

Claim 9(1); Page 9; 48pp; German.

This invention describes a novel method for detecting microorganisms (A)

of importance in brewing which comprises treating a sample with at least

two primers (P1) that hybridize to a consensus region in the nucleic acid

of (A), at least part of the microbial nucleic acid is amplified, the

amplicon is treated with at least one probe (P2) that hybridizes

specifically with a sequence common to all (A) or specific for one or

more families, genera or species, and any formation of hybrids is

detected. The method is used to detect, identify and/or characterize

microorganisms in beer or brewing materials, particularly for detecting

contamination. The method may detect the entire range of contaminating

microbes, either as a general test for contamination or as a test

specific for particular genera or (sub) species. It is quicker than known

microbiological methods, and can detect several organisms in the same

sample, including organisms not presently recognized as contaminants. The

method provides an early indication of contamination and can be automated

for high throughput analysis

Sequence 267 BP; 77 A; 51 C; 77 G; 62 T; 0 U; 0 Other;

95	13	61.9	444	6	ABN68526	Abn68526 Streptococcus
96	13	61.9	455	9	AC117009	AC117009 DNA clone
97	13	61.9	456	8	AB252858	AB252858 Aspergillus
98	13	61.9	458	8	ABX43980	ABX43980 Bovine ES
99	13	61.9	489	10	ADG37805	ADG37805 Aspergillus
100	13	61.9	499	4	AA133114	AA133114 Probe #18

ALIGNMENTS

RESULT 3

AAZ43884 standard; cDNA; 2215 BP.

AAZ43884;

10-MAR-2000 (first entry)

C. vicina LSP-2 cDNA.

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

AT11phorin; calliphorin; ABP; receptor-binding domain; plant protection;

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 12:43:29 ; Search time 163.364 Seconds
(without alignment)
6056.719 Million cell updates/sec

Title: US-10-088-666-21

Sequence: 1 ccaagtcacacacgtagctgtc 21

Scoring table: OLIGO-WGC
Gapex 60.0, Gapext 60.0

Searched: 4526729 segs, 23644849745 residues

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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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8	16	76.2	40689	2	AC129903	AC129903 Ciona sav
9	16	76.2	107579	8	AC016162	AC016162 Arabidops
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16	16	76.2	228453	2	AC146729	AC146729 Ootlemur
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18	16	76.2	261162	1	AE017257	AE017257 Wolbachia
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23	15	71.4	1390	3	AK114505	AK114505 Ciona int
24	15	71.4	3375	3	AY216495	AY216495 Toxoplasm
25	15	71.4	4407	14	HB6DNAFOL	HB6DNAFOL
26	15	71.4	4549	3	CBIFHD1	CBIFHD1
27	15	71.4	10060	3	AY216496	AY216496 Toxoplasm
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31	15	71.4	37400	5	AF022814	AF022814 Fugu rubr
32	15	71.4	38491	14	HB6TMEERH	HB6TMEERH
33	15	71.4	68167	5	AL731656	AL731656 Zebrafish
34	15	71.4	72443	2	AC019973	AC019973 Drosophill
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 C 95 14 66.7 2744 14 CLCVAJ455 AJ002455 Cotton 1e
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 C 97 14 66.7 2964 8 AY372822 Magnapor
 C 98 14 66.7 3168 5 AY247207 Gasterost
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ALIGNMENTS

RESULT 1
 LOCUS AX105749 21 bp DNA linear PAT 30-APR-2001
 DEFINITION Sequence 21 from Patent WO0123605.
 ACCESSION AX105749
 VERSION AX105749.1 GI:13921762
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS Pandke, M., Gasch, A. and Berghof, K.
 TITLE Method and nucleic acids for determining the presence of
 JOURNAL micro-organisms specific to the brewing process
 PATENT Patent: WO 0123605-A 21 05-APR-2001;
 Biorecon Diagnostics GmbH (DE)
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 DEFINITION Sequence 1 from Patent WO0123605.
 ACCESSION AX105729
 VERSION AX105729.1 GI:13921742
 KEYWORDS
 SOURCE
 ORGANISM

Lactobacillus brevis
 Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 Lactobacillus.

REFERENCE
 AUTHORS Pandke, M., Gasch, A. and Berghof, K.
 TITLE Method and nucleic acids for determining the presence of
 JOURNAL micro-organisms specific to the brewing process
 PATENT Patent: WO 0123605-A 1 05-APR-2001;
 Biorecon Diagnostics GmbH (DE)

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 DEFINITION Calliphora vicina hexamerin LSP-2 mRNA, complete cds.
 ACCESSION U89789
 VERSION U89789.1 GI:1890113
 KEYWORDS
 SOURCE
 ORGANISM

Calliphora vicina
 Calliphora vicina
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Oestroidea; Calliphoridae; Calliphora.

REFERENCE
 AUTHORS Burmester, T., Kolling, C., Schroer, B. and Scheller, K.
 TITLE Complete sequence, expression, and evolution of the hexamerin LSP-2
 JOURNAL of Calliphora vicina
 INSECT BIOCHEM. MOL. BIOL. 28 (1), 11-22 (1998)
 MEDLINE
 PUBMED
 98275862
 9612935
 2 (bases 1 to 2215)
 REFERENCE
 AUTHORS Scheller, K., Koelling, C., Schroer, B. and Burmester, T.
 TITLE Direct Submission
 JOURNAL Submitted (17-FEB-1997) Biologie du Developpement, Institut Jacques
 Monod, 2 place Jussieu, Paris 75005, France
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ORIGIN

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RESULT 4
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 DEFINITION Brassica napus resistance-related marker.
 ACCESSION AF149254
 VERSION AF149254.1 GI:14317917
 KEYWORDS
 SOURCE
 ORGANISM

Brassica napus (rape)
 Brassica napus


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CDS
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
Lactobacillus.  
REFERENCE  
AUTHORS Fandke,M., Gasch,A. and Berghof,K.  
TITLE Method and nucleic acids for determining the presence of  
micro-organisms specific to the brewing process  
JOURNAL Patent: WO 012605-A 1 05-Apr-2001;  
FEATURES Biotechn Diagnostica GmbH (DE)  
source Location/Qualifiers  
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RESULT 3                 AY327391                 4692 bp        DNA         linear        VRT 23-JUN-2004  
LOCUS                    AY327391  
DEFINITION Basilleuterus rivularis NADH dehydrogenase subunit 2, cytochrome  
oxidase subunit I, cytochrome oxidase subunit II, ATP-synthase 8,  
and ATP-synthase 6 genes, complete cds; mitochondrial.  
VERSION AY327391  
KEYWORDS AY327391.1 GI:39979797  
SOURCE .  
ORGANISM mitochondrion Basilleuterus rivularis [neotropical river warbler]  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauromorpha; Aves; Neognathae; Passeriformes; Passeriidae;  
Fringillidae; Emberizinae; Basilleuterus.  
1 (bases 1 to 4692)  
Loveite,I.J.  
Molecular phylogeny and plumage signal evolution in a trans Andean  
mol. Phylogenet. Evol. 32 (2), 512-523 (2004)
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JOURNAL JOURNAL PUBLISHED REFERENCE AUTHORS TITLE  
SUBMITTED Direct Submission  
Submitted (20-JUN-2003) Laboratory of Ornithology, Cornell  
University, 159 Sapsucker Woods Road, Ithaca, NY 14850, USA  
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DB	1555 CCAAGTCACCAACTAGTTGT 1575			
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LOCUS	AY327393			
DEFINITION	Basilleterus fulvicauda NAH dehydrogenase subunit 2, cytochrome			
	oxidase subunit I, cytochrome oxidase subunit II, ATP-synthase 8,			
	and ATP-synthase 6 genes, complete cds; mitochondrial.			
ACCESSION	AY327393			
VERSION	AY327393.1 GI:39979809			
KEYWORDS				
SOURCE				
ORGANISM				
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	Arcosauaria; Aves; Neognathae; Passeriformes; Passeroidea;			
	Fringillidae; Emberizinae; Basilleterus.			

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 7250342

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	18	90.0	465	US-10-425-115-45008	Sequence 45008, A
3	17.4	87.0	593	US-10-029-386-1346	Sequence 1346, A
4	17.4	87.0	6200	US-09-795-061-3	Sequence 3, Appl1
5	17	85.0	127267	US-10-322-281-797	Sequence 797, Appl
6	16.8	84.0	175561	US-10-017-721-3	Sequence 3, Appl1
7	16.8	84.0	175561	US-10-235-192A-48	Sequence 48, Appl1
8	16.8	84.0	1230025	US-10-289-762-1	Sequence 1, Appl1
9	16.8	84.0	1503841	US-09-795-668-1	Sequence 1, Appl1
10	16.8	84.0	1503841	US-09-795-668-1	Sequence 1, Appl1
11	16.8	84.0	1503841	US-09-795-668-1	Sequence 1, Appl1
12	16.4	82.0	255	US-10-149-736-7	Sequence 7, Appl1

C 13	16.4	82.0	465	9	US-09-974-300-3058	Sequence 3058, Ap
C 14	16.4	82.0	688	13	US-10-027-632-102170	Sequence 102170,
C 15	16.4	82.0	688	13	US-10-027-632-102171	Sequence 102171,
C 16	16.4	82.0	688	15	US-10-027-632-102170	Sequence 102170,
C 17	16.4	82.0	688	15	US-10-027-632-102171	Sequence 102171,
C 18	16.4	82.0	1340	10	US-09-845-416-11	Sequence 11, Appl1
C 19	16.4	82.0	1667	10	US-09-845-416-11	Sequence 11, Appl1
C 20	16.4	82.0	1991	10	US-09-845-416-3	Sequence 3, Appl1
C 21	16.4	82.0	2022	17	US-10-437-963-57769	Sequence 57769, A
C 22	16.4	82.0	3446	10	US-09-845-416-14	Sequence 14, Appl1
C 23	16.4	82.0	3510	10	US-09-845-416-12	Sequence 12, Appl1
C 24	16.4	82.0	3531	10	US-09-845-416-10	Sequence 10, Appl1
C 25	16.4	82.0	3858	10	US-09-845-416-9	Sequence 9, Appl1
C 26	16.4	82.0	3999	10	US-09-845-416-6	Sequence 6, Appl1
C 27	16.4	82.0	4182	10	US-09-845-416-2	Sequence 2, Appl1
C 28	16.4	82.0	4414	10	US-09-845-416-32	Sequence 32, Appl1
C 29	16.4	82.0	4476	10	US-09-845-416-31	Sequence 31, Appl1
C 30	16.4	82.0	4498	10	US-09-845-416-30	Sequence 30, Appl1
C 31	16.4	82.0	4825	10	US-09-845-416-29	Sequence 29, Appl1
C 32	16.4	82.0	4848	10	US-09-845-416-35	Sequence 35, Appl1
C 33	16.4	82.0	4966	10	US-09-845-416-28	Sequence 28, Appl1
C 34	16.4	82.0	4990	10	US-09-845-416-36	Sequence 36, Appl1
C 35	16.4	82.0	5060	10	US-09-845-416-36	Sequence 36, Appl1
C 36	16.4	82.0	5149	10	US-09-845-416-27	Sequence 27, Appl1
C 37	16.4	82.0	5339	15	US-10-149-736-40	Sequence 40, Appl1
C 38	16.4	82.0	5417	15	US-10-149-736-39	Sequence 39, Appl1
C 39	16.4	82.0	5462	15	US-10-149-736-41	Sequence 41, Appl1
C 40	16.4	82.0	8689	15	US-10-149-736-42	Sequence 42, Appl1
C 41	16.4	82.0	11058	10	US-09-845-416-1	Sequence 1, Appl1
C 42	16.4	82.0	11443	15	US-10-149-736-44	Sequence 44, Appl1
C 43	16.4	82.0	12057	15	US-10-149-736-47	Sequence 47, Appl1
C 44	16.4	82.0	13957	9	US-09-782-378A-22	Sequence 22, Appl1
C 45	16.4	82.0	13957	9	US-09-880-107-2284	Sequence 2284, Ap

ALIGNMENTS

RESULT 1
US-09-795-061-1, Application US/09795061
; Sequence 1, Appl1
; Publication No. US20030166842A1
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S
; APPLICANT: Imamura, Yasutada
; TITLE OF INVENTION: Pro-Alpha 3 (V) Collagen Genes
; FILE REFERENCE: 960296, 96781
; CURRENT APPLICATION NUMBER: US/09/795, 061
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6109
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)..(5298)
US-09-795-061-1

Query Match 92.0%; Score 18.4; DB 10; Length 6109;
Best Local Similarity 95.0%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;
QY 1 GAGGGAAGAAGTCTCTTAT 20
Db 4907 GAGGGAAGAAGTCTCTTAT 4926
RESULT 2
US-10-425-115-45008
; Sequence 45008, Application US/10425115
; Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovall, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 45008
LENGTH: 465
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_141051C.1
US-10-425-115-45008

Query Match 90.0%; Score 18; DB 18; Length 465;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGAGAGAGTCTCTAT 20
DB 439 GGGAGAGAGTCTCTAT 456

RESULT 3
US-10-029-386-1346
Sequence 1346, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AEWICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 1346
LENGTH: 593
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC013816.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.56
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.51
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.43
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.36
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.56
OTHER INFORMATION: SWISSPROT HIT: Q00083, EVALU8 5.80e+00
OTHER INFORMATION: EST HUMAN HIT: S6539472.1, EVALU8 8.30e-01
OTHER INFORMATION: NT HIT: AJ314911.1, EVALU8 2.20e+00
US-10-029-386-1346

Query Match 87.0%; Score 17.4; DB 15; Length 593;
Best Local Similarity 94.7%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AGGAGAGAGTCTCTAT 20
DB 524 AGGAGAGAGTCTCTAT 542

RESULT 4
US-09-795-061-3
Sequence 3, Application US/09795061
Publication No. US20030166842A1

GENERAL INFORMATION:
APPLICANT: Greenspan, Daniel S
APPLICANT: Imamura, Yasutada
TITLE OF INVENTION: Pro-Alpha 3(V) Collagen Genes
FILE REFERENCE: 960296.96781
CURRENT APPLICATION NUMBER: US/09/795,061
CURRENT FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 3
LENGTH: 6200
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (87)..(5321)
US-09-795-061-3

Query Match 87.0%; Score 17.4; DB 10; Length 6200;
Best Local Similarity 94.7%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGAGAGAGTCTCTTA 19
DB 4927 GAGGAGAGAGTCTCTTA 4945

RESULT 5
US-10-322-281-797
Sequence 797, Application US/10322281
Publication No. US20040126762A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 52945200100
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 797
LENGTH: 127767
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(127767)
OTHER INFORMATION: n = A,T,C or G
US-10-322-281-797

Query Match 85.0%; Score 17; DB 17; Length 127767;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGAAGAGTCTCTAT 20
DB 5129 GGAAGAGTCTCTAT 5145

RESULT 6
US-10-017-721-3/C
Sequence 3, Application US/10017721
Publication No. US20030096248A1
GENERAL INFORMATION:
APPLICANT: McCarthy, Jeanette
APPLICANT: Daley, George
APPLICANT: Boik, Stacey
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
FILE REFERENCE: MMI-003
CURRENT APPLICATION NUMBER: US/10/017,721
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/317,033
PRIOR FILING DATE: 2001-09-04

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:14 ; Search time 8.64865 Seconds
(without alignments)
1643.659 Million cell updates/sec

Title: US-10-088-666-74

Perfect score: 20

Sequence: 1 gagggagaagtcctcttat 20

Scoring table: IDENTITY NUC

Gapop 10_0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18.4	92.0	6109	4	US-09-795-061-1 Sequence 1, Appli
2	17.4	82.0	6200	4	US-09-795-061-3 Sequence 3, Appli
3	16.8	84.0	1230025	4	US-09-198-452A-1 Sequence 1, Appli
4	16.4	82.0	5952	4	US-09-687-875A-1 Sequence 1, Appli
5	16.4	82.0	13977	4	US-09-484-970B-60 Sequence 60, Appli
6	15.8	79.0	239	3	US-09-443-184-18 Sequence 18, Appli
7	15.8	79.0	244	3	US-09-443-184-19 Sequence 19, Appli
8	15.8	79.0	267	3	US-09-443-184-17 Sequence 17, Appli
9	15.8	79.0	3001	4	US-09-539-333D-156 Sequence 156, App
10	15.8	79.0	3182	1	US-07-797-556-5 Sequence 5, Appli
11	15.8	79.0	3182	1	US-07-943-843-1 Sequence 1, Appli
12	15.8	79.0	3182	1	US-08-347-003-1 Sequence 1, Appli
13	15.8	79.0	3591	1	US-07-943-843-5 Sequence 5, Appli
14	15.8	79.0	3591	1	US-08-347-003-5 Sequence 5, Appli
15	15.8	79.0	26000	4	US-09-843-376-10 Sequence 10, Appli
16	15.4	77.0	4519	4	US-08-976-259-6 Sequence 6, Appli
17	15.4	77.0	4519	4	US-09-956-004-6 Sequence 6, Appli
18	15.4	77.0	4712	4	US-09-221-017B-577 Sequence 577, App
19	15.4	77.0	148567	4	US-09-801-876B-3 Sequence 3, Appli
20	15.4	77.0	148567	4	US-10-254-869-3 Sequence 3, Appli
21	15.2	76.0	2344	3	US-08-893-852A-2 Sequence 2, Appli
22	15.2	76.0	2432	1	US-08-339-214-29 Sequence 29, Appli
23	15.2	76.0	2808	2	US-07-708-962-1 Sequence 1, Appli
24	15.2	76.0	2808	2	US-08-153-721B-1 Sequence 1, Appli
25	15.2	76.0	3394	4	US-09-427-154-1 Sequence 1, Appli
26	15.2	76.0	3498	4	US-09-350-982C-4 Sequence 4, Appli
27	15.2	76.0	3515	4	US-09-221-017B-824 Sequence 824, App

ALIGNMENTS

28	15.2	76.0	3797	4	US-09-696-668-1 Sequence 1, Appli
29	15.2	76.0	3816	4	US-09-696-668-2 Sequence 2, Appli
30	15.2	76.0	4275	4	US-09-972-115A-5 Sequence 5, Appli
31	15.2	76.0	4512	4	US-09-350-982C-3 Sequence 3, Appli
32	15.2	76.0	5075	4	US-09-799-451-556 Sequence 556, App
33	15.2	76.0	6018	4	US-09-849-602-111 Sequence 11, Appli
34	15.2	76.0	6114	4	US-09-543-681A-1366 Sequence 1366, Ap
35	15.2	76.0	128779	4	US-09-497-855A-38 Sequence 38, Appli
36	15	75.0	1166	4	US-09-325-932A-139 Sequence 139, App
37	14.8	74.0	597	2	US-08-332-766A-19 Sequence 19, Appli
38	14.8	74.0	990	4	US-09-134-000C-1245 Sequence 1245, Ap
39	14.8	74.0	1025	3	US-08-643-212-17 Sequence 17, Appli
40	14.8	74.0	1025	3	US-08-643-212-19 Sequence 19, Appli
41	14.8	74.0	1025	3	US-08-643-212-21 Sequence 21, Appli
42	14.8	74.0	1025	3	US-08-643-212-23 Sequence 23, Appli
43	14.8	74.0	1025	3	US-08-643-212-25 Sequence 25, Appli
44	14.8	74.0	1025	3	US-08-643-212-27 Sequence 27, Appli
45	14.8	74.0	1025	3	US-08-643-212-29 Sequence 29, Appli

RESULT 1
US-09-795-061-1
; Sequence 1, Application US/09795061
; Patent No. 6759528
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S
; TITLE OF INVENTION: Pro-Alpha 3(V) Collagen Genes
; FILE REFERENCE: 960296, 96781
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6109
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)..(5298)
US-09-795-061-1

Query Match 92.0%; Score 18.4; DB 4; Length 6109;
Best Local Similarity 95.0%; Prod. No. 5.7;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGGAAGAGTCTCTTAT 20
Db 4907 GAGGGAAGAGTCTCTTAT 4926

RESULT 2
US-09-795-061-3
; Sequence 3, Application US/09795061
; Patent No. 6759528
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S
; TITLE OF INVENTION: Pro-Alpha 3(V) Collagen Genes
; FILE REFERENCE: 960296, 96781
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 6200
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

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LOCATION: (87) .. (5321)
US-09-795-061-3
Query Match 87.0%; Score 17.4; DB 4; Length 6200;
Best Local Similarity 94.7%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGAGAAAGTCTCTTA 19
DB 4927 GAGGAGAAAGTCTCTTA 4945

RESULT 3
US-09-198-452A-1/c
Sequence 1, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
LENGTH: 1230025
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1) .. (15000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (15001) .. (30000)
OTHER INFORMATION: n=a or c or g or t
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (525001) .. (540000)
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NAME/KEY: misc_feature
LOCATION: (540001) .. (555000)
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NAME/KEY: misc_feature
LOCATION: (555001) .. (570000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (570001) .. (585000)
```


CC microbes, either as a general test for contamination or as a test
CC specific for particular genera or (sub)species. It is quicker than known
CC microbiological methods, and can detect several organisms in the same
CC sample, including organisms not presently recognized as contaminants. The
CC method provides an early indication of contamination and can be automated
CC for high throughput analysis

XX Sequence 20 BP; 6 A; 2 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGAGAGAGTCTCTAT 20
Db 1 GAGGAGAGAGTCTCTAT 20

RESULT 2
AAF61566
ID AAF61566 standard; DNA; 267 BP.

XX AAF61566;

XX 02-JUL-2001 (first entry)

XX Lactobacillus brevis 23S rRNA-spacer-5S rRNA DNA fragment.

XX 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.

XX Lactobacillus brevis.

XX DB19945964-A1.

XX 05-APR-2001.

XX 24-SEP-1999; 99DE-01045964.

XX 24-SEP-1999; 99DE-01045964.

XX (BIOT-) BIOTECON DIAGNOSTICS GMBH.

XX Fandke M, Gasch A, Berghof K;

XX WPI; 2001-246136/26.

XX Detecting contaminating microorganisms in brewing, by nucleic acid
PT amplification and hybridization, either non-specific or genus- or species
PT -specific.

XX Claim 9(1); Page 9; 48pp; German.

XX This invention describes a novel method for detecting microorganisms (A)
CC of importance in brewing which comprises treating a sample with at least
CC two primers (P1) that hybridize to a consensus region in the nucleic acid
CC of (A), at least part of the microbial nucleic acid is amplified, the
CC amplicon is treated with at least one probe (P2) that hybridizes
CC specifically with a sequence common to all (A) or specific for one or
CC more families, genera or species, and any formation of hybrids is
CC detected. The method is used to detect, identify and/or characterize
CC microorganisms in beer or brewing materials, particularly for detecting
CC contamination. The method may detect the entire range of contaminating
CC microbes, either as a general test for contamination or as a test
CC specific for particular genera or (sub)species. It is quicker than known
CC microbiological methods, and can detect several organisms in the same
CC sample, including organisms not presently recognized as contaminants. The
CC method provides an early indication of contamination and can be automated
CC for high throughput analysis

XX Sequence 267 BP; 77 A; 51 C; 77 G; 62 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 6.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGAGAGAGTCTCTAT 20
Db 154 GAGGAGAGAGTCTCTAT 173

RESULT 3
ABN26443
ID ABN26443 standard; cDNA; 337 BP.

XX ABN26443;

XX 24-JUN-2002 (first entry)

XX Human ORFX polynucleotide sequence SEQ ID NO:21363.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
XX hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
XX degenerative disorder; osteoarthritis; neurodegenerative disorder;
XX cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
XX hypertension; hypothyroidism; cholesterol ester storage disease;
XX immune deficiency; immune disorder; infectious disease;
XX autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
XX myasthenia gravis; gene; ss.

XX Homo sapiens.

XX W0200192523-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US010836.

XX 30-MAY-2000; 2000US-0206132P.

XX 29-AUG-2000; 2000US-0228716P.

XX (CURA-) CURAGEN CORP.

XX Shinketsu RA, Leach MD;

XX WPI; 2002-106308/14.

XX P-PSDB; ABP106591.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders.

XX Disclosure; SEQ ID NO 21363; 1037pp; English.

XX The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification)). ABN15762 to ABN27253 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC syndrome in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage. N.B. The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:13 ; Search time 156.216 Seconds
(without alignments)
6054.391 Million cell updates/sec

Title: US-10-088-666-74

Perfect score: 20

Sequence: 1 GAGGGAAGAGTCTCTTAT 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_srs:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	AX105802	AX105802 Sequence
2	20	100.0	267	AX105729	AX105729 Sequence
3	18.4	92.0	337	CO455603	CO455603 Sequence
4	18.4	92.0	6076	AF272661	AF272661 Rattus no
5	18.4	92.0	6109	AX239611	AX239611 Sequence
6	18.4	92.0	6109	AF176645	AF176645 Mus muscu
7	18.4	92.0	155793	AC102821	AC102821 Mus muscu
8	18.4	92.0	182757	AC122484	AC122484 Mus muscu
9	18	90.0	229813	AC117613	AC117613 Mus muscu
10	17.4	87.0	1907	CO723784	CO723784 Sequence
11	17.4	87.0	6200	AX239613	AX239613 Sequence
12	17.4	87.0	6200	AF177941	AF177941 Homo sapi
13	17.4	87.0	6368	AX405643	AX405643 Sequence
14	17.4	87.0	39969	HS164519	HS164519 Human DNA
15	17.4	87.0	110000	AC109525_0	AC109525_0
16	17.4	87.0	157410	AC013816	AC013816 Homo sapi
17	17.4	87.0	166701	AC011457	AC011457 Homo sapi
18	17.4	87.0	166711	AC006116	AC006116 Homo sapi
19	17.4	87.0	168119	AC068686	AC068686 Homo sapi

20	17.4	87.0	169136	2	BX511100
21	17.4	87.0	175406	2	AC087128
22	17.4	87.0	180962	2	AC121560
23	17.4	87.0	192944	2	AC146902
24	17.4	87.0	194427	9	AC093153
25	17.4	87.0	207004	5	AL954695
26	17.4	87.0	207596	2	AC141506
27	17.4	87.0	208657	2	AC046179
28	17.4	87.0	210636	2	AC105070
29	17.4	87.0	217548	2	BX571726
30	17.4	87.0	223843	10	AC102595
31	17.4	87.0	229448	2	AC113690
32	17.4	87.0	229563	10	AC024957
33	17.4	87.0	235662	2	AC126709
34	17.4	87.0	237019	2	AC094443
35	17.4	87.0	239870	2	AC094970
36	17.4	87.0	243689	2	AC128281
37	17.4	87.0	259178	2	AC108971
38	17.4	87.0	271189	2	AC128515
39	17.4	87.0	304851	2	AC121044
40	17	85.0	101707	2	AC150157
41	17	85.0	128809	9	AC021648
42	17	85.0	172825	2	AC020614
43	17	85.0	187221	10	AC117229
44	17	85.0	192734	10	AL928798
45	17	85.0	227515	2	AC150065

ALIGNMENTS

RESULT 1	AX105802	20 bp	DNA	linear	PAT 30-APR-2001
LOCUS	AX105802	Sequence 74 from Patent WO0123605.			
DEFINITION	AX105802				
ACCESSION	AX105802.1	GI:13921815			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
1	Fandke, M., Gasch, A. and Berghof, K.				
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
1..20					
/organism="synthetic construct"					
/mol_type="unassigned DNA"					
/db_xref="taxon:32630"					
/note="spezifische Sequenz für Lactobacillus brevis"					
ORIGIN					
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Best Local Similarity		100.0%;	Pred. No. 1.3e+02;		
Matches	20;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	1	GAGGGAAGAGTCTCTTAT	20		
Db	1	GAGGGAAGAGTCTCTTAT	20		
RESULT 2					
AX105729					
LOCUS	AX105729	267 bp	DNA	linear	PAT 30-APR-2001
DEFINITION	Sequence 1 from Patent WO0123605.				
ACCESSION	AX105729				
VERSION	AX105729.1	GI:13921742			
KEYWORDS					
SOURCE					
ORGANISM					
1	Lactobacillus brevis				
2	Lactobacillus brevis				

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.

1
Fandke, M., Gasch, A. and Berghof, K.
Method and nucleic acids for determining the presence of
micro-organisms specific to the brewing process
Patent: WO 0123605-A 1 05-APR-2001;
Biotechon Diagnostis GmbH (DE)
Location/Qualifiers

1..267
/organism="Lactobacillus brevis"
/mol_type="unassigned DNA"
/db_xref="taxon:1580"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGAGAGAGTTCTCTTAT 20
154 GAGGAGAGAGTTCTCTTAT 173

RESULT 3
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CO455603 337 bp DNA linear PAT 30-JAN-2004
Sequence 21363 from Patent WO0192523.
CO455603
CO455603.1 GI:41422032

1
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Shinkets, R.A. and Leach, M.D.
Human polynucleotides and polypeptides encoded thereby
Patent: WO 0192523-A 21363 06-DEC-2001;
Curagen Corporation (US)
Location/Qualifiers

1..337
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 92.0%; Score 18.4; DB 6; Length 337;
Best Local Similarity 95.0%; Pred. No. 4,8e-02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGAGAGAGTTCTCTTAT 20
131 GAGGAGAGAGTTCTCTTAT 150

RESULT 4
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AF272661 6076 bp mRNA linear ROD 11-SEP-2000
Rattus norvegicus alpha 4 type V collagen mRNA, complete cds.
AF272661
AF272661.1 GI:8568093

1
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 6076)
Chernousov, M.A., Rothblum, K., Tyler, W.A., Stahl, R.C. and Carey, D.J.
Schwann cells synthesize type V collagen that contains a novel
alpha 4 chain. Molecular cloning, biochemical characterization, and
high affinity heparin binding of alpha 4(V) collagen

JOURNAL
MEDLINE
PubMed
AUTHORS
TITLE
JOURNAL
FEATURES
source

J. Biol. Chem. 275 (36), 28208-28215 (2000)
20428740
10852920
2 (bases 1 to 6076)
Chernousov, M.A., Rothblum, K.N., Tyler, W.A., Stahl, R.C. and
Carey, D.J.
Direct Submission
Submitted (26-MAY-2000) Weis Center for Research, Penn State
College of Medicine, 100 N. Academy Ave., Danville, PA 17822, USA
Location/Qualifiers

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/db_xref="taxon:10116"
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/db_xref="GI:8568094"

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TLVDCERPMPWEGGPRVTSAGLTVWGTOLGSESPGDIOSLLIPDOALQAC
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GAPENQTSLLHPTETKSPHLPPTPTPLAITTYVMGNATVLOGLDSTETEMTP
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PYGQGLGPGPDGIGLQGPPTGQAGGPRGLGPRGPRPLRPGVTSDDGAPGA
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PKGDRNPGLPGRGDEDEGQKPEGLGADSPGAPAGKGLVPCLPYRRRPG
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GSPAGKEGKGLPLQGPGRPPGPKPPGQKDGIPGPRGREGELFGQGTGPPGAG
VAGPAGKVDVGLGPRGPRGPPGPRGGLGIGRAGAKGLPLSILGKEGPPG
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WIDPNGCARDAFVFCNFTAGGTCVLPDKKFTVRLASMRKRGVSTFRGKX
FSYVDADGSPVAVVVLITFLKLSAAHQHFTVTCNSAAMDASGDHRSIRFGGTN
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ORIGIN

Query Match 92.0%; Score 18.4; DB 10; Length 6076;
Best Local Similarity 95.0%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGAGAGAGTTCTCTTAT 20
4875 GAGGAGAGAGTTCTCTTAT 4894

RESULT 5
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX239611 6109 bp DNA linear PAT 26-SEP-2001
Sequence 1 from Patent WO0164871.
AX239611
AX239611.1 GI:15797284

1
Mus musculus (house mouse)
Mus musculus

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:13 ; Search time 417.042 Seconds
(without alignments)
2184.416 Million cell updates/sec

Title: US-10-088-666-73

Sequence: 1 tcgaataatcgaataatcctag 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.8	83.2	717	9	AC296763 Mus muscu
2	20.2	80.8	460	9	AQ489622 RPT-11-2
3	19.8	79.2	887	9	CNS06W55
4	19.4	77.6	848	8	AZ683885 ENTL32TF
5	19.4	77.6	877	8	CC141515 NDL.32X2
6	19.4	77.6	898	8	BH133066 ENTPC66TR
7	19.4	77.6	900	8	BH147215 ENTQPC4TR
8	19.4	77.6	900	8	BH136672 ENTNA82TR
9	19.2	76.8	214	9	CR398469 Arabidops
10	19.2	76.8	277	9	CG148828 PUFKVA6TB
11	19.2	76.8	307	9	CL257264 ZMMBBD061
12	19.2	76.8	340	6	CD324627 Str-Pus37
13	19.2	76.8	382	9	CE401158 tigr-gss-
14	19.2	76.8	386	9	CE624663 tigr-gss-
15	19.2	76.8	390	8	BZ632366 PUFKVA6TB
16	19.2	76.8	405	8	CG148831 PUFKVA6TB
17	19.2	76.8	409	8	BZ632406 PUFKVA6TB
18	19.2	76.8	413	8	BZ632362 PUFKVA6TB
19	19.2	76.8	424	8	BH170927 SALX_0035
20	19.2	76.8	464	9	CE853568 tigr-gss-
21	19.2	76.8	482	7	CC0517136 tigr-gss-
22	19.2	76.8	482	7	CC0517136 tigr-gss-
23	19.2	76.8	568	9	CE345622 tigr-gss-
24	19.2	76.8	570	9	CE313026 tigr-gss-

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
25	19.2	76.8	583	9	CE029479	tigr-gss-				
26	19.2	76.8	601	9	CE378676	tigr-gss-				
27	19.2	76.8	630	9	CE407289	tigr-gss-				
28	19.2	76.8	639	9	CE397029	tigr-gss-				
29	19.2	76.8	646	9	CE717195	tigr-gss-				
30	19.2	76.8	685	9	CE745651	tigr-gss-				
31	19.2	76.8	709	9	CL827541	tigr-gss-				
32	19.2	76.8	711	9	AG123355	OR_CBA04				
33	19.2	76.8	742	9	CE459772	tigr-gss-				
34	19.2	76.8	743	9	CE224657	tigr-gss-				
35	19.2	76.8	757	9	CL757754	OR_BBA012				
36	19.2	76.8	833	9	CG048515	PUTLOC0TB				
37	19.2	76.8	911	8	BZ829021	PUCB037TD				
38	19.2	76.0	888	9	CG965204	MEMMD88TF				
39	18.8	75.2	402	8	AQ207867	HS_3138_A				
40	18.8	75.2	405	1	AI872073	t261911.x				
41	18.8	75.2	506	9	CG696733	MUGO_CH25				
42	18.8	75.2	574	8	AQ466749	HS_5170_A				
43	18.8	75.2	595	9	CE163486	tigr-gss-				
44	18.8	75.2	628	6	CD004668	VIB040E09				
45	18.8	75.2	630	9	CR323914	Medicago				

FEATURES

source

AG296763 717 bp DNA linear GSS 02-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-073H13.T7, genomic survey
sequence.
AG296763
AG296763.1 GI:47869717
GSS.
Mus musculus molossinus
Mus musculus molossinus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Hattori, M., Toyoda, A., Noguichi, H., Kojima, T. and Sakaki, Y.
BAC end Sequences of Library MSMg01
Unpublished
2 (bases 1 to 717)
Hattori, M., Toyoda, A., Noguichi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-chou, Tsukuba, Ibaraki, Japan, 305-0874, Japan
Tel: 81-45-503-9111, Fax: 81-45-503-9170
E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kunhya Abe (abe@rcc.riken.jp).
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyada, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rcc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBAC3.6
R Site 1 : BclRI
R Site 2 : BclRI.
Location/Qualifiers
1. 717
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ORIGIN

Query Match 83.2%; Score 20.8; DB 9; Length 717;
 Best Local Similarity 91.7%; Pred. No. 5.3e+02;
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Db 507 TCGAGATTAATGATATATCTA 484

1 TCGAGATTAATGATATATCTA 24
 |||||

RESULT 2
 A0489622/c 460 bp DNA linear GSS 24-APR-1999
 LOCUS RPCT-11-231C16.TV RPCT-11 Homo sapiens genomic clone
 DEFINITION RPCT-11-231C16, genomic survey sequence.
 ACCESSION A0489622
 VERSION A0489622.1 GI:4675496
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 460)
 Zhao,S., Adams,M.D., Niernan,W., Malek,J., de Jong,P. and
 Venter,J.C.
 Use of BAC End Sequences from Library RPCT-11 for Sequence-Ready
 Map Building
 Unpublished (1997)
 Other_GSS: RPCT-11-231C16.TV
 Contact: Shanying Zhao, William Niernan, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeet@ig.org
 Clones are derived from the human BAC library RPCT-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buhalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buhalo.edu/ordering) or from
 Research Genet cs (info@resgen.com). BAC end search page:
 http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers
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 RPCT11 Human Male BAC Library"

ORIGIN

Query Match 80.8%; Score 20.2; DB 8; Length 460;
 Best Local Similarity 88.0%; Pred. No. 9.2e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 250 TCGAGATTAATGATATATCTAG 226

1 TCGAGATTAATGATATATCTAG 25
 |||||

RESULT 3
 CNS06W55/c 887 bp DNA linear GSS 06-JUL-2001
 LOCUS T3 end of clone AX0AA028C03 of library AX0AA from strain CBS 7064
 DEFINITION of Pichia farinosa, genomic survey sequence.

ACCESSION AL417999
 VERSION AL417999.1 GI:12200400
 KEYWORDS GSS.
 SOURCE Pichia farinosa
 ORGANISM Pichia farinosa
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 Saccharomycetales; Saccharomycetaceae; Pichia.
 1 (bases 1 to 887)
 Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
 Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
 de Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Lorente,B.,
 Malpertuy,A., Neuvéglise,C., Ozier-Kalogiropoulos,O., Potier,S.,
 Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Jouvel,M.,
 Wincker,P. and Weissenbach,J.
 Genomic exploration of the hemiascomycetous yeasts: 1. A set of
 yeast species for molecular evolution studies
 FEMS Lett. 487 (1), 3-12 (2000)

1152876
 20584725
 2 (bases 1 to 887)
 de Montigny,J., Spehner,C., Souciet,J., Tekala,F., Dujon,B.,
 Wincker,P., Artiguenave,F. and Potier,S.
 Genomic exploration of the hemiascomycetous yeasts: 15. Pichia
 sorbitophila
 FEMS Lett. 487 (1), 87-90 (2000)

20584725
 1152890
 3 (bases 1 to 887)
 Genoscope.
 Direct Submission
 Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage,
 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
 seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 This GSS is part of a random genomic sequencing program of thirteen
 yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
 exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxi,
 Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
 lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
 angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
 Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
 5 kb were prepared and both extremities were sequenced. See
 keywords for description of this sequence and for the sequence of
 the other extremity of this insert.

Location/Qualifiers
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 /strain="CBS 7064"
 /db_xref="taxon:4920"
 /clone_lib="AX0AA028C03"
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 /note="end : T3"

ORIGIN

Query Match 79.2%; Score 19.8; DB 9; Length 887;
 Best Local Similarity 84.0%; Pred. No. 1.3e+03;
 Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 850 TCGAGATTAATTAATATATATG 826

1 TCGAGATTAATTAATATATATG 25
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RESULT 4
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 LOCUS ENTLP327P Entamoeba histolytica Shared DNA Entamoeba histolytica
 DEFINITION genomic, genomic survey sequence.
 ACCESSION A2683885
 VERSION A2683885.1 GI:11821031
 KEYWORDS GSS.
 SOURCE Entamoeba histolytica
 ORGANISM Entamoeba histolytica

GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:50:19 ; Search time 43.1682 Seconds
(without alignments)
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Title: US-10-088-666-73

Perfect score: 25

Sequence: 1 tcgagataatgataatctag 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.8	75.2	228	14	US-10-016-349A-108
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3	18.6	74.4	1206	18	US-10-425-115-119404
4	18.4	73.6	1891	17	US-10-437-963-45894
5	18.2	72.8	332	15	US-10-369-493-29816
6	18.2	72.8	588	15	US-10-029-386-6066
7	18.2	72.8	638	17	US-10-767-701-26220
8	18.2	72.8	2179	9	US-09-070-927A-468
9	18.2	72.8	163701	17	US-10-322-281-439
10	18.2	72.8	1830121	14	US-10-329-960-1
11	18.2	72.8	1830121	16	US-10-329-670-1
12	18.2	72.8	1830121	18	US-10-158-865-1

C	13	18	72.0	1190	9	US-09-070-927A-714	Sequence 714, App
C	14	18	72.0	5962	15	US-10-311-455-1259	Sequence 1259, App
C	15	17.8	71.2	493	16	US-10-424-599-74009	Sequence 74009, A
C	16	17.8	71.2	1118	13	US-10-027-632-118527	Sequence 118527, A
C	17	17.8	71.2	1118	13	US-10-027-632-118528	Sequence 118528, A
C	18	17.8	71.2	1118	13	US-10-027-632-118529	Sequence 118529, A
C	19	17.8	71.2	1118	15	US-10-027-632-118528	Sequence 118528, A
C	20	17.8	71.2	3393	15	US-10-128-714-203	Sequence 203, App
C	21	17.6	70.4	160	9	US-09-294-098B-3755	Sequence 3755, App
C	22	17.6	70.4	204	18	US-10-425-115-36493	Sequence 36493, A
C	23	17.6	70.4	332	18	US-10-425-115-104351	Sequence 104351, A
C	24	17.6	70.4	578	9	US-09-867-701-6635	Sequence 6635, App
C	25	17.6	70.4	549	16	US-10-425-114-34850	Sequence 34850, A
C	26	17.6	70.4	601	13	US-10-027-632-18543	Sequence 18543, A
C	27	17.6	70.4	601	15	US-10-027-632-18543	Sequence 18543, A
C	28	17.6	70.4	615	13	US-10-027-632-282529	Sequence 282529, A
C	29	17.6	70.4	615	15	US-10-027-632-282529	Sequence 282529, A
C	30	17.6	70.4	771	16	US-10-425-114-1795	Sequence 1795, App
C	31	17.6	70.4	998	16	US-10-425-114-19489	Sequence 19489, A
C	32	17.6	70.4	1001	15	US-10-170-097-112	Sequence 112, App
C	33	17.6	70.4	1001	15	US-10-170-097-112	Sequence 112, App
C	34	17.6	70.4	1141	16	US-10-425-114-712	Sequence 712, App
C	35	17.6	70.4	1163	16	US-10-425-114-19232	Sequence 19232, A
C	36	17.6	70.4	1298	16	US-10-425-114-6794	Sequence 6794, App
C	37	17.6	70.4	1298	18	US-10-425-115-90866	Sequence 90866, A
C	38	17.6	70.4	1359	16	US-10-424-599-35445	Sequence 35445, A
C	39	17.6	70.4	1370	16	US-10-425-114-1104	Sequence 1104, App
C	40	17.6	70.4	1375	16	US-10-425-114-5129	Sequence 5129, App
C	41	17.6	70.4	1388	16	US-10-425-114-1028	Sequence 1028, App
C	42	17.6	70.4	1389	16	US-10-425-114-3166	Sequence 3166, App
C	43	17.6	70.4	1389	16	US-10-425-114-15767	Sequence 15767, A
C	44	17.6	70.4	1389	16	US-10-425-114-35028	Sequence 35028, A
C	45	17.6	70.4	1393	16	US-10-425-114-1203	Sequence 1203, App

ALIGNMENTS

RESULT 1
US-10-016-349A-108
; Sequence 108, Application US/10016349A
; Publication No. US20030064378A1
; GENERAL INFORMATION:
; APPLICANT: Recipon, Herve
; APPLICANT: Sun, Yongming
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods relating to Lung Specific Genes and Prote
; FILE REFERENCE: DEX-0243
; CURRENT APPLICATION NUMBER: US/10/016,349A
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/243,459
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 228
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-016-349A-108
Query Match 75.2%; Score 18.8; DB 14; Length 228;
Best Local Similarity 90.9%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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RESULT 2
US-10-016-349A-109/c

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; Sequence 109, Application US/10016349A
; Publication No. US20030064378A1
; GENERAL INFORMATION:
; APPLICANT: Recipon, Herve
; APPLICANT: Sun, Yongming
; APPLICANT: Chen, Sei-yu
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods relating to Lung Specific Genes and Prot
; FILE REFERENCE: DEX-0243
; CURRENT APPLICATION NUMBER: US/10/016,349A
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/243,459
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 244
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; ORGANISM: Homo sapiens
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; Best Local Similarity 90.9%; Pred. No. 1.2e+03;
; Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGAATATTGAATATATCTG 25
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RESULT 3
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; Sequence 119404, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 119404
; LENGTH: 1206
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_40380C.1
; US-10-425-115-119404

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Query Match 74.4%; Score 18.6; DB 18; Length 1206;
Best Local Similarity 84.0%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGGAATATTGAATATATCTAG 25
DB 271 TCGGATATTGATGATCTAG 247

RESULT 4
US-10-437-963-45894/C
; Sequence 45894, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 45894
; LENGTH: 1891
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48814C.1
; US-10-437-963-45894
; Query Match 73.6%; Score 18.4; DB 17; Length 1891;
; Best Local Similarity 95.0%; Pred. No. 1.8e+03;
; Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 AGAATATTGAATATATCT 23
DB 1795 AGAATATTGATATATCT 1776

RESULT 5
US-10-369-493-29816/C
; Sequence 29816, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 29816
; LENGTH: 332
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; US-10-369-493-29816
; Query Match 72.8%; Score 18.2; DB 15; Length 332;
; Best Local Similarity 87.0%; Pred. No. 1.8e+03;
; Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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GenCore version 5.1.6
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CM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:14 ; Search time 10.8108 Seconds

(without alignments)
1643.699 Million cell updates/sec

Title: US-10-088-666-73

Perfect score: 25

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	18.2	72.8	468	US-09-134-000C-316	Sequence 316, App
C 4	18.2	72.8	1830121	US-09-557-884-1	Sequence 1, Appli
C 5	18.2	72.8	1830121	US-09-643-990A-1	Sequence 1, Appli
C 6	18.2	72.8	1830121	US-10-329-960-1	Sequence 1, Appli
C 7	17.6	70.4	103	US-09-313-284A-1728	Sequence 1728, Ap
C 8	17.6	70.4	1001	US-09-313-294A-2255	Sequence 2255, Ap
C 9	17.6	70.4	1001	US-09-641-638-111	Sequence 111, App
C 10	17.6	70.4	1001	US-09-641-638-112	Sequence 112, App
C 11	17.6	70.4	1001	US-10-170-097-111	Sequence 111, App
C 12	17.6	70.4	1001	US-10-170-097-112	Sequence 112, App
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C 15	17.4	69.6	1830121	US-10-329-960-1	Sequence 1, Appli
C 16	17.2	68.8	441	US-09-710-279-1795	Sequence 1795, Ap
C 17	17.2	68.8	462	US-09-134-001C-2294	Sequence 2294, Ap
C 18	17.2	68.8	2943	US-09-710-279-3983	Sequence 3983, Ap
C 19	17.2	68.8	3249	US-09-710-279-3622	Sequence 3622, Ap
C 20	17.2	68.8	3442	US-09-710-279-4030	Sequence 4030, Ap
C 21	17	68.0	1557	US-09-270-767-28519	Sequence 28519, A
C 22	17	68.0	1585	US-09-270-767-28996	Sequence 28996, A
C 23	17	68.0	1907	US-09-270-767-13100	Sequence 13100, A
C 24	17	68.0	2970	US-09-710-279-2593	Sequence 2593, Ap
C 25	17	68.0	3128	US-09-270-767-12706	Sequence 12706, A
C 26	17	68.0	3271	US-09-710-279-4142	Sequence 4142, Ap
C 27	17	68.0	3461	US-09-710-279-3713	Sequence 3713, Ap

C 28	16.8	67.2	222	US-09-328-352-1425	Sequence 1425, Ap
C 29	16.8	67.2	564	US-09-248-796A-2085	Sequence 2085, Ap
C 30	16.8	67.2	759	US-09-710-279-1031	Sequence 1031, Ap
C 31	16.8	67.2	834	US-09-248-796A-2317	Sequence 2317, Ap
C 32	16.8	67.2	1386	US-09-134-001C-2474	Sequence 2474, Ap
C 33	16.8	67.2	2301	US-09-710-279-419	Sequence 419, App
C 34	16.8	67.2	2634	US-09-710-279-4189	Sequence 4189, App
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C 37	16.8	67.2	3321	US-09-710-279-4058	Sequence 4058, Ap
C 38	16.8	67.2	3352	US-09-107-532A-3026	Sequence 3026, Ap
C 39	16.8	67.2	3602	US-09-710-279-3430	Sequence 3430, Ap
C 40	16.8	67.2	3825	US-09-710-279-3799	Sequence 3799, Ap
C 41	16.8	67.2	6968	US-09-710-279-759	Sequence 759, App
C 42	16.8	67.2	7215	US-09-134-001C-627	Sequence 627, App
C 43	16.6	66.4	434	US-09-513-999C-10571	Sequence 10571, A
C 44	16.6	66.4	735	US-09-107-532A-1648	Sequence 1648, Ap
C 45	16.6	66.4	3025	US-08-956-171B-178	Sequence 178, App

ALIGNMENTS

RESULT 1
US-08-936-107A-8/c
Sequence 8, Application US/08936107A
Patent No. 6403306
GENERAL INFORMATION:
APPLICANT: Stephens, David S.
TITLE OF INVENTION: Serogroup-Specific Nucleotide Sequences
TITLE OF INVENTION: In the Molecular Typing of Bacterial Isolates and the
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESSES:
ADDRESS: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,107A
FILING DATE: 23-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/827,622
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Caruthers, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 77-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8080
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5064 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULAR TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 479..1597
FEATURE:
NAME/KEY: CDS
Sequence 3713, Ap

LOCATION: 1599..3236
FEATURE:
NAME/KEY: CDS
LOCATION: 3309..4052
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NAME/KEY: CDS
LOCATION: 4054..4917
US-08-936-107A-8

Query Match 73.6%; Score 18.4; DB 4; Length 5064;
Best Local Similarity 95.0%; Pred. No. 86;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGAGATATGATGATATA 20
DB 3612 TCGATATATGATGATATA 3593

RESULT 2
US-09-134-000C-317
Sequence 317, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patent version 3.1
SEQ ID NO 317
LENGTH: 234
TYPE: DNA
ORGANISM: Enterococcus faecalis
US-09-134-000C-317

Query Match 72.8%; Score 18.2; DB 4; Length 234;
Best Local Similarity 87.0%; Pred. No. 11e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCGAGATATGATGATATATCT 23
DB 191 TCGAGATATGATGATATATCT 213

RESULT 3
US-09-134-000C-316/C
Sequence 316, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patent version 3.1
SEQ ID NO 316
LENGTH: 468
TYPE: DNA
ORGANISM: Enterococcus faecalis
US-09-134-000C-316

Query Match 72.8%; Score 18.2; DB 4; Length 468;
Best Local Similarity 87.0%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCGAGATATGATGATATATCT 23
DB 211 TCGAGATATGATGATATATCT 189

RESULT 4
US-09-557-884-1
Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments thereof, and uses thereof

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS V6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Query Match 72.8%; Score 18.2; DB 4; Length 1830121;
Best Local Similarity 87.0%; Pred. No. 86;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGAGATATGATGATATATCTA 24
DB 35497 CGAGATATGATGATATCTTA 354519

RESULT 5
US-09-643-990A-1
Sequence 1, Application US/09643990A
Patent No. 6528289
GENERAL INFORMATION:
APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments thereof, and uses thereof
NUMBER OF SEQUENCES: 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:13 ; Search time 48.4985 Seconds
(without alignments)
2705.971 Million cell updates/sec

Title: US-10-088-666-73

Sequence: 1 tcgagaataatgataataatctag 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1980s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	5	AAF61638 Lactobac
2	25	100.0	267	5	AAF61566 Lactobac
3	18.8	75.2	228	8	ABO82965 Human lun
4	18.8	75.2	1324	8	ABO82966 Human lun
5	18.4	73.6	5064	2	AAV69110 Neisseria
6	18.4	73.6	25426	8	ADA41645 Human sec
7	18.4	73.6	25426	8	ACC50940 Human sec
8	18.4	73.6	25426	10	ADD38155 CDNA clon
9	18.4	73.6	234	10	ADH82432 Enterococ
10	18.2	72.8	468	10	ADH82431 Enterococ
11	18.2	72.8	588	12	ACH72871 Human gen
12	18.2	72.8	2179	2	AAAX1405 Enterococ
13	18.2	72.8	2179	6	ABSS9200 Enterococ
14	18.2	72.8	22620	4	ABLO7500 Drosophi
15	18.2	72.8	22620	4	AAAT4063_03
16	18.2	72.8	1190	2	AAAX1651 Enterococ
17	18.2	72.0	1190	6	ABSS9446 Enterococ
18	18.2	72.0	5962	6	ABL33286 Human imm
19	17.8	71.2	1151	10	ADCO8440 Rice DNA
20	17.8	71.2	3393	8	ABT17845 Aspergill
21	17.8	71.2	3393	8	ABT17845 Aspergill

22	17.6	70.4	103	10	ABX83278	Abx83278 Corn ear-
23	17.6	70.4	160	6	ABL74381	ABL74381 Corn tass
24	17.6	70.4	210	10	ABX83795	Abx83795 Corn ear-
25	17.6	70.4	349	6	ABL83657	ABL83657 Human ova
26	17.6	70.4	1001	3	AAC57478	AAC57478 Human ova
27	17.6	70.4	1001	3	AAC57477	AAC57477 Arabidops
28	17.6	70.4	1486	3	AAC39081	AAC39081 Arabidops
29	17.6	70.4	2076	8	ACA33067	ACA33067 Prokaryot
30	17.6	70.4	2079	4	AAS52961	AAS52961 Enterococ
31	17.6	70.4	2345	2	ABL22259	ABL22259 Drosophi
32	17.6	70.4	3212	2	AAV03313	AAV03313 Archaeogl
33	17.6	70.4	3212	10	AAJ56488	AAJ56488 Phosphata
34	17.6	70.4	5387	4	ABL21402	ABL21402 Drosophi
35	17.6	70.4	6032	6	AAJ56331	AAJ56331 Chemical
36	17.6	70.4	8042	4	ABL22258	ABL22258 Drosophi
37	17.6	70.4	14429	6	ABL34242	ABL34242 Human imm
38	17.6	70.4	14429	6	ABO67097	ABO67097 Human ang
39	17.6	70.4	23989	4	AAK72555	AAK72555 Human imm
40	17.6	70.4	110000	2	AAK20248_00	AAK20248 Borrelia
41	17.6	70.4	157030	12	ADQ47194	ADQ47194 DNA seque
42	17.6	70.4	312477	12	ADP69744	ADP69744 Human ROC
43	17.4	69.6	324	12	ADH35221	ADH35221 Human TGF
44	17.4	69.6	558	4	AAJ53233	AAJ53233 Haemophil
45	17.4	69.6	558	8	ACA34026	ACA34026 Prokaryot

ALIGNMENTS

RESULT 1
ID AAF61638 standard; DNA: 25 BP.
AC AAF61638;
DT 02-JUL-2001 (first entry)
XX Lactobacillus brevis 23S rRNA/5S rRNA specific probe SRQ ID 73.
XX 23S rRNA, 5S rRNA; detection; probe; brewing; beer; contamination; ss.
XX Lactobacillus brevis.
XX DE19945964-A1.
XX 05-APR-2001.
XX 24-SEP-1999; 99DE-01045964.
XX 24-SEP-1999; 99DE-01045964.
XX 24-SEP-1999; 99DE-01045964.
XX (BIOT-) BIOTECOM DIAGNOSTICS GMBH.
XX Fandke M, Gasch A, Bergthof K;
XX WPI; 2001-246136/26.
XX Detecting contaminating microorganisms in brewing, by nucleic acid
XX amplification and hybridization, either non-specific or genus- or species
XX specific.
XX Claim 9(i); Page 17; 48pp; German.
XX
XX This invention describes a novel method for detecting microorganisms (A)
XX of importance in brewing which comprises treating a sample with at least
XX two primers (P1) that hybridize to a consensus region in the nucleic acid
XX of (A), at least part of the microbial nucleic acid is amplified, the
XX amplicon is treated with at least one probe (P2) that hybridizes
XX specifically with a sequence common to all (A) or specific for one or
XX more families, genera or species, and any formation of hybrids is
XX detected. The method is used to detect, identify and/or characterize
XX microorganisms in beer or brewing materials, particularly for detecting
XX contamination. The method may detect the entire range of contaminating

CC microbes, either as a general test for contamination or as a test
 CC specific for particular genera or (sub)species. It is quicker than known
 CC microbiological methods, and can detect several organisms in the same
 CC sample, including organisms not presently recognized as contaminants. The
 CC method provides an early indication of contamination and can be automated
 CC for high throughput analysis

XX Sequence 25 BP; 11 A; 2 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 5; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGAGATATATGATATATCTAG 25
 DB 1 TCGAGATATATGATATATCTAG 25

RESULT 2
 ID AAF61566 standard; DNA; 267 BP.

XX AAF61566;

DT 02-JUL-2001 (first entry)

DE Lactobacillus brevis 23S rRNA-spacer-5S rRNA DNA fragment.

XX 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.

XX Lactobacillus brevis.

XX DE19945964-A1.

XX 05-APR-2001.

XX 24-SEP-1999; 99DE-01045964.

XX 24-SEP-1999; 99DE-01045964.

XX (BIOT-) BIOTECON DIAGNOSTICS GMBH.

XX Fandke M, Gasch A, Berghof K;

XX WPI; 2001-246136/26.

XX Detecting contaminating microorganisms in brewing, by nucleic acid

XX amplification and hybridization, either non-specific or genus- or species

XX -specific.

XX Claim 9(i); Page 9; 48pp; German.

XX This invention describes a novel method for detecting microorganisms (A)
 CC of importance in brewing which comprises treating a sample with at least
 CC two primers (P1) that hybridize to a consensus region in the nucleic acid
 CC of (A), at least part of the microbial nucleic acid is amplified, the
 CC amplicon is treated with at least one probe (P2) that hybridizes
 CC specifically with a sequence common to all (A) or specific for one or
 CC more families, genera or species, and any formation of hybrids is
 CC detected. The method is used to detect, identify and/or characterize
 CC microorganisms in beer or brewing materials, particularly for detecting
 CC contamination. The method may detect the entire range of contaminating
 CC microbes, either as a general test for contamination or as a test
 CC specific for particular genera or (sub)species. It is quicker than known
 CC microbiological methods, and can detect several organisms in the same
 CC sample, including organisms not presently recognized as contaminants. The
 CC method provides an early indication of contamination and can be automated
 CC for high throughput analysis

XX Sequence 267 BP; 77 A; 51 C; 77 G; 62 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 5; Length 267;
 Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGAGATATATGATATATCTAG 25
 DB 125 TCGAGATATATGATATATCTAG 149

RESULT 3
 ID ABQ82965 standard; cDNA; 228 BP.

XX ABQ82965;

DT 15-JAN-2003 (first entry)

DE Human lung specific nucleic acid (LSNA) SEQ ID NO:108.

XX Human; lung specific gene; lung specific nucleic acid; LSG; LSNA; LSP;

XX lung specific protein; lung cancer; vaccine; gene therapy; gene; ss.

XX Homo sapiens.

XX WO20027236-A2.

XX 03-OCT-2002.

XX 26-OCT-2001; 2001WO-US050385.

XX 26-OCT-2000; 2000US-0243459P.

XX (DIAD-) DIADEXUS INC.

XX Recipon H, Sun Y, Chen S, Liu C, Turner LR;

XX WPI; 2003-018930/01.

XX New isolated nucleic acid molecule, useful for treating lung cancer, and
 XX diagnosing or monitoring the presence of metastases of lung cancer in a
 XX patient.

XX Claim 1; Page 204; 262pp; English.

XX The present invention describes a isolated human lung specific nucleic
 CC acid (LSNA) molecule comprising a sequence selected from ABQ82858 to
 CC ABQ82993, which encodes a human lung specific protein (LSP) sequence
 CC selected from ABP54165 to ABP54272. Also described: (1) a method for
 CC determining the presence of a LSNA or LSP in a sample; (2) a vector
 CC comprising the novel nucleic acid; (3) a host cell comprising the vector
 CC of (2); (4) producing a polypeptide encoded by the novel nucleic acid;
 CC (5) an isolated polypeptide produced by the method of (4); (6) an
 CC antibody or its fragment that specifically binds to the polypeptide of
 CC (5); (7) diagnosing and monitoring the presence of metastases of lung
 CC cancer in a patient; (8) treating a patient with lung cancer; or (9) a
 CC vaccine comprising the polypeptide of (5) or the novel nucleic acid. The
 CC human LSNA and LSP sequences have cytosolic activity, and can be used in
 CC vaccines and gene therapy. The LSNA and LSP sequences can also be used
 CC for treating lung cancer, and diagnosing or monitoring the presence of
 CC metastases of lung cancer in a patient

XX Sequence 228 BP; 83 A; 29 C; 50 G; 66 T; 0 U; 0 Other;

Query Match 75.2%; Score 18.8; DB 8; Length 228;
 Best Local Similarity 90.9%; Pred. No. 6e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGAATATGATATATCTAG 25
 DB 17 AGAATATGATATATCTAG 38

RESULT 4
 ID ABQ82965/c
 ID ABQ82966 standard; cDNA; 1324 BP.

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:13 ; Search time 195.27 Seconds
(without alignments)
6054.391 Million cell updates/sec

Title: us-10-088-666-73

Perfect score: 25

Sequence: 1 tcgagatcattgataatctag 25

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Lasting first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_per:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6	AX105801 Sequence
2	25	100.0	267	6	AX105729 Sequence
3	20.4	81.6	110000	2	AC141815_0
4	20.2	80.8	64701	2	AC079132
5	20.2	80.8	178448	9	AC099805
6	19.8	79.2	153768	2	AC113566
7	19.8	79.2	238427	2	AC113234
8	19.4	77.6	119113	5	EX005199
9	19.4	77.6	145011	2	CR548634
10	19.4	77.6	149163	2	AC073835
11	19.4	77.6	154412	9	HS144P13
12	19.4	77.6	195130	9	AL355832
13	19.2	76.8	482	11	CR377191
14	19.2	76.8	1131	10	AF012235
15	19.2	76.8	35291	5	EX649551
16	19.2	76.8	83537	5	EX004805
17	19.2	76.8	92624	8	AC003000
18	19.2	76.8	103029	9	AC133537
19	19.2	76.8	123406	8	AC120508

c	20	19.2	76.8	135129	2	AC148864	AC148864	Canis fam
c	21	19.2	76.8	137923	5	EX640536	EX640536	Zebrafish
c	22	19.2	76.8	139257	2	AC150028	AC150028	Canis fam
c	23	19.2	76.8	152841	2	AL929463	AL929463	Danio rer
c	24	19.2	76.8	153438	2	AC117959	AC117959	Rattus no
c	25	19.2	76.8	171061	2	EX950177	EX950177	Danio rer
c	26	19.2	76.8	174846	2	AC141676	AC141676	Apis mell
c	27	19.2	76.8	177722	2	EX928747	EX928747	Danio rer
c	28	19.2	76.8	189219	9	AC092982	AC092982	Homo sapi
c	29	19.2	76.8	189355	2	AC053539	AC053539	Homo sapi
c	30	19.2	76.8	194717	2	AC113424	AC113424	Homo sapi
c	31	19.2	76.8	202587	2	AC119862	AC119862	Mus muscu
c	32	19.2	76.8	202922	2	EX901959	EX901959	Danio rer
c	33	19.2	76.8	222615	5	AL929345	AL929345	Zebrafish
c	34	19.2	76.8	226614	2	EX957306	EX957306	Danio rer
c	35	19.2	76.8	268324	5	AL954838	AL954838	Zebrafish
c	36	19.2	76.8	342116	2	AC130918	AC130918	Rattus no
c	37	19.2	76.8	348465	2	AC131165	AC131165	Rattus no
c	38	19	76.0	164921	2	AC150864	AC150864	Bos tauru
c	39	19	76.0	226341	2	AC130020	AC130020	Rattus no
c	40	18.8	75.2	228	6	AX566136	AX566136	Sequence
c	41	18.8	75.2	787	3	AY573636	AY573636	Drosophila
c	42	18.8	75.2	787	3	AY573639	AY573639	Drosophila
c	43	18.8	75.2	788	3	AY573632	AY573632	Drosophila
c	44	18.8	75.2	788	3	AY573633	AY573633	Drosophila
c	45	18.8	75.2	788	3	AY573634	AY573634	Drosophila

ALIGNMENTS

RESULT 1	AX105801	25 bp	DNA	linear	PAT 30-APR-2001
LOCUS	AX105801	Sequence 73 from Patent WO0123605.			
DEFINITION	AX105801				
ACCESSION	AX105801.1	GI:13921814			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
Query Match	100.0%	Score 25;	DB 6;	Length 25;	
Best Local Similarity	100.0%	Pred. No. 43;			
Matches	25;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	TCGAGATATATTGAATATATCTAG	25		
Db	1	TCGAGATATATTGAATATATCTAG	25		
RESULT 2	AX105729	267 bp	DNA	linear	PAT 30-APR-2001
LOCUS	AX105729	Sequence 1 from Patent WO0123605.			
DEFINITION	AX105729				
ACCESSION	AX105729.1	GI:13921742			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					

Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.

REFERENCE
1
Fardke, M., Gasch, A. and Berghof, K.
TITLE
Method and nucleic acids for determining the presence of
micro-organisms specific to the brewing process
JOURNAL
Patent: WO 0123605-A 1 05-Apr-2001;
Biotecon Diagnostics GmbH (DE)
Location/Qualifiers
1..267
/organism="Lactobacillus brevis"
/mol_type="unassigned DNA"
/db_xref="taxon:1580"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY
1 TCGAGATATGATATATATCTAG 25
125 TCGAGATATGATATATCTAG 149

Db

RESULT 3
AC141815 0/c
Sequence split into 4 fragments LOCUS AC141815 Accession AC141815
Fragment Name Begin End
AC141815_0 1 110000
AC141815_1 100001 210000
AC141815_2 200001 310000
AC141815_3 300001 409619
AC141815 409619 bp DNA linear HTG 19-MAR-2003
LOCUS AC141815
DEFINITION Apis mellifera clone CH224-61C4, WORKING DRAFT SEQUENCE, 94
unordered pieces.
AC141815
AC141815.1 GI:29123999
HTG; HTGS PHASE1; HTGS DRAFT.
KEYWORDS
SOURCE
ORGANISM
Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apidae; Apis.
1 (bases 1 to 409619)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Albrooks, S.L., Amaralunga, H.C., Are, J.R., Ayala, M., Banks, T.,
Barbiera, J., Benton, J., Blum, K., Blankenburg, K., Bonnin, D.,
Boucek, J., Bowie, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Butrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, U., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Dem, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Hawlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hughes, M., Hollway, C., Hollins, B.,
Homer, R., Howard, S., Huber, J., Hulys, S., Joudah, S.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Kovach, J., Kovar, C.,
Karlsen, E., Kelly, S., Khan, U., King, L., Lewis, L.C., Lewis, L.,
Kraevic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Louisedge, H.,
Lozdo, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Marindale, A., Martinez, E.,
Massey, E., Mahoney, E., McLeod, M.P., Meador, M., Mei, G., Metzger, S.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Moran, M., Morris, S.,
Mosier, M., Neal, D., Newton, J., Nohbhat, K., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogun, M., Okunolu, G.,

ORGANISM
TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL
COMMENT

Organye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G.,
Scherer, S., Scott, G., Shen, H., Shoochian, N., Sisson, I.,
Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Swalek, A., Tabor, P., Tameris, A., Tameris, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Teifod, B., Thomas, N., Thomas, S.,
Uemami, K., Vasquez, L., Vera, V., Villalob, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wiczysk, R., Wooden, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.
Direct Submission
2 (bases 1 to 409619)
Unpublished
Morley, K.C.
Submitted (19-MAR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.bsgc.bcm.tmc.edu/>
Contact: hgc-help@bcm.tmc.edu
----- Project Information
Center project name: AMBL
Center clone name: CH224-61C4
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 371769 bases at least Q40
Consensus quality: 383951 bases at least Q30
Consensus quality: 392893 bases at least Q20
Estimated insert size: 375080; sum-of-coverage estimation
Quality coverage: 3x in Q20 bases; sum-of-coverage estimation

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently
consists of 94 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 1189: contig of 1189 bp in length
1190 1289: gap of unknown length
1290 2420: contig of 1131 bp in length
2421 2520: gap of unknown length
2521 3713: contig of 1193 bp in length
3714 3813: gap of unknown length
3814 4963: contig of 1150 bp in length
4964 5063: gap of unknown length
5064 6387: contig of 134 bp in length
6388 6487: gap of unknown length
6488 7548: contig of 1061 bp in length
7549 7648: gap of unknown length
7649 9094: contig of 1446 bp in length
9095 9194: gap of unknown length
9195 10256: contig of 1062 bp in length
10257 11389: gap of unknown length
11390 11489: contig of 1033 bp in length
11490 12816: gap of unknown length
12817 12916: gap of 1327 bp in length
12917 13951: contig of 1035 bp in length
13952 14051: gap of unknown length
14052 15422: contig of 1371 bp in length
15423 15522: gap of unknown length

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:13 ; Search time 350.315 Seconds
(without alignments)
2184.416 Million cell updates/sec

Title: US-10-088-666-21

Perfect score: 21

Sequence: 1 ccaagtcacacagctagttgt 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
3: gb_hrc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	17.8	84.8	214	2	BE478105
5	17.8	84.8	218	2	BE486429
6	17.8	84.8	261	7	CR383046
7	17.8	84.8	290	7	CF614527
8	17.8	84.8	313	5	AM426583
9	17.8	84.8	337	5	BO640947
10	17.8	84.8	369	2	BE488687
11	17.8	84.8	387	2	BE475991
12	17.8	84.8	413	1	AV613476
13	17.8	84.8	418	7	CF362784
14	17.8	84.8	420	6	CB168898
15	17.8	84.8	421	2	BF230248
16	17.8	84.8	424	2	BE588467
17	17.8	84.8	427	1	AV618453
18	17.8	84.8	432	6	CB165949
19	17.8	84.8	442	2	BE476579
20	17.8	84.8	450	2	BE483083
21	17.8	84.8	451	4	BM432873
22	17.8	84.8	451	5	BP110601
23	17.8	84.8	454	6	CB221784
24	17.8	84.8	471	2	BE487090

25	17.8	84.8	472	2	BE481873	BE481873
26	17.8	84.8	477	1	AJ691187	AJ691187
27	17.8	84.8	477	2	BE483952	BE483952
28	17.8	84.8	479	4	BM431900	BM431900
29	17.8	84.8	493	2	BE483642	BE483642
30	17.8	84.8	494	4	BM432022	BM432022
31	17.8	84.8	495	5	BP107620	BP107620
32	17.8	84.8	498	2	BE481915	BE481915
33	17.8	84.8	502	2	BE485555	BE485555
34	17.8	84.8	509	2	BE482287	BE482287
35	17.8	84.8	512	2	BE481721	BE481721
36	17.8	84.8	512	2	BE487910	BE487910
37	17.8	84.8	513	2	BE476202	BE476202
38	17.8	84.8	513	2	BE480446	BE480446
39	17.8	84.8	515	1	AV667257	AV667257
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41	17.8	84.8	519	4	BG680664	BG680664
42	17.8	84.8	522	2	BE481271	BE481271
43	17.8	84.8	524	2	BP110809	BP110809
44	17.8	84.8	525	4	BM431956	BM431956
45	17.8	84.8	534	1	AV606713	AV606713

ALIGNMENTS

RESULT 1
BH542735
LOCUS
DEFINITION
BOGXU95TR BOGX Brassica oleracea genomic clone BOGXU95, genomic survey sequence.
ACCESSION
BH542735
VERSION
BH542735.1 GI:17794516
KEYWORDS
GSS.
SOURCE
Brassica oleracea
ORGANISM
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 779)
Town,C.D., Van Aken,S., Uteback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
JOURNAL
Unpublished (2001)
COMMENT
Other GSSs: BOGXU95TF
Contact: Chris Town

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES

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1..779
Location/Qualifiers
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 356 CCAAGTCACACAGCTAGTT 373

RESULT 2
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DEFINITION 256171 MRC BSM Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF430206
VERSION BF430206.1 GI:11442303
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos
1 (bases 1 to 197)
Warren, W.C., Tao, N., Allison, T., Wagner, S., Mathiasagan, N.,
Kata, S., Johnson, J., Smith, T.P.L., and Womack, J.
A survey of genes transcribed in bovine skeletal muscle
Unpublished (2000)
Contact: Smith TP
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithe@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: GGAACAGCTATGACCATG
BACKWARD: GTTTCCTCAGCAGC
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/clone_id="MARC BSM"
/note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;
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made from skeletal muscle of a two year old Holstein cow."

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Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAAGTCAACAGCTAGTTGT 21
DB 41 CCAATCTACACGTAAGTTGT 61

RESULT 3
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DEFINITION 161290 BARC SBOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE477537
VERSION BE477537.1 GI:9597070
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos
1 (bases 1 to 204)
Sonstegard, T., Capuco, A.V., White, J., Van Tassel, C.P.,
Connor, E.B., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, U.
Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
22135956

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
22135956

PUBMED 12140684
CONTACT: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@ps1.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGCAGC
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ORIGIN
Query Match 84.8%; Score 17.8; DB 2; Length 204;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAAGTCAACAGCTAGTTGT 21
DB 138 CCAATCTACACGTAAGTTGT 158

RESULT 4
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DEFINITION 162195 BARC SBOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE478105
VERSION BE478105.1 GI:9597638
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos
1 (bases 1 to 214)
Sonstegard, T., Capuco, A.V., White, J., Van Tassel, C.P.,
Connor, E.B., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, U.
Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
22135956

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
22135956

CONTACT: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@ps1.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGCAGC
Plate: 6 row: A column: 2
Seq primer: ATTACCTCCTCAAG.

Tue Nov 16 16:09:54 2004

us-10-088-666-21.rnpb

Page 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
3127.876 Million cell updates/sec

Title: US-10-088-666-21

Perfect score: 21

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues 7250342

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	17.8	84.8	242	9	US-09-960-352-13451
6	17.8	84.8	247	9	US-09-960-352-183
7	17.8	84.8	292	9	US-09-960-352-7737
8	17.8	84.8	301	9	US-09-960-352-86
9	17.8	84.8	308	9	US-09-960-352-10392
10	17.8	84.8	340	9	US-09-960-352-2761
11	17.8	84.8	341	9	US-09-960-352-2191
12	17.8	84.8	342	9	US-09-960-352-11482

13	17.8	84.8	348	9	US-09-960-352-9403	Sequence 9403, Ap
14	17.8	84.8	358	9	US-09-960-352-6472	Sequence 8472, Ap
15	17.8	84.8	360	9	US-09-960-352-2079	Sequence 2079, Ap
16	17.8	84.8	360	9	US-09-960-352-12857	Sequence 12857, A
17	17.8	84.8	366	9	US-09-960-352-8659	Sequence 8659, Ap
18	17.8	84.8	366	9	US-09-960-352-14094	Sequence 14094, A
19	17.8	84.8	368	9	US-09-960-352-4223	Sequence 4223, Ap
20	17.8	84.8	378	9	US-09-960-352-2966	Sequence 2966, Ap
21	17.8	84.8	382	9	US-09-960-352-215	Sequence 215, App
22	17.8	84.8	385	9	US-09-960-352-10641	Sequence 10641, A
23	17.8	84.8	391	9	US-09-960-352-10595	Sequence 10595, A
24	17.8	84.8	395	9	US-09-960-352-2505	Sequence 2505, A
25	17.8	84.8	398	9	US-09-960-352-7013	Sequence 7013, Ap
26	17.8	84.8	399	9	US-09-960-352-9396	Sequence 9396, Ap
27	17.8	84.8	404	9	US-09-960-352-179	Sequence 179, App
28	17.8	84.8	404	9	US-09-960-352-7795	Sequence 7795, Ap
29	17.8	84.8	405	9	US-09-960-352-1246	Sequence 1246, Ap
30	17.8	84.8	406	9	US-09-960-352-12380	Sequence 12380, A
31	17.8	84.8	407	9	US-09-960-352-9846	Sequence 9846, Ap
32	17.8	84.8	416	9	US-09-960-352-11517	Sequence 11517, A
33	17.8	84.8	417	9	US-09-960-352-10053	Sequence 10053, A
34	17.8	84.8	419	9	US-09-960-352-15059	Sequence 15059, Ap
35	17.8	84.8	420	9	US-09-960-352-6117	Sequence 6117, Ap
36	17.8	84.8	427	9	US-09-960-352-7803	Sequence 7803, Ap
37	17.8	84.8	430	9	US-09-960-352-5911	Sequence 5911, Ap
38	17.8	84.8	458	9	US-09-960-352-9145	Sequence 9145, Ap
39	17.8	84.8	553	11	US-09-876-143-840	Sequence 840, App
40	17.8	84.8	586	11	US-09-876-143-140	Sequence 140, App
41	17.8	84.8	606	11	US-09-876-143-744	Sequence 744, App
42	17.8	84.8	641	11	US-09-876-143-197	Sequence 197, App
43	17.8	84.8	641	11	US-09-876-143-285	Sequence 285, App
44	17.8	84.8	690	11	US-09-876-143-791	Sequence 791, App
45	17.8	84.8	957	11	US-09-876-143-1436	Sequence 1436, Ap

ALIGNMENTS

RESULT 1
US-09-960-352-4229
Sequence 4229, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21 (10298) C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 4229
LENGTH: 207
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 18-LIB34-062-Q1-E1-E5
US-09-960-352-4229

Query Match 84.8%; Score 17.8; DB 9; Length 207;
Best Local Similarity 90.5%; Pred. No. 62;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAAGTCACACAGTAGTGT 21
Db 162 CCAATCTACACAGTAGTGT 182

RESULT 2
US-09-960-352-2061
Sequence 2061, Application US/09960352
Patent No. US20020137139A1

GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2061
; LENGTH: 211
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 09-LIB34-062-Q1-E1-C9
US-09-960-352-2061

Query Match 84.8%; Score 17.8; DB 9; Length 211;
Best Local Similarity 90.5%; Pred. No. 62;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCAAGTCAACAGCTAGTTGT 21
Db 124 CCAATCTCAACAGCTAGTTGT 144

RESULT 3
US-09-960-352-4220
; Sequence 4220, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4220
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 18-LIB34-051-Q1-E1-B5
US-09-960-352-4220

Query Match 84.8%; Score 17.8; DB 9; Length 229;
Best Local Similarity 90.5%; Pred. No. 63;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCAAGTCAACAGCTAGTTGT 21
Db 144 CCAATCTCAACAGCTAGTTGT 164

RESULT 4
US-09-960-352-13451
; Sequence 13451, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112

; SEQ ID NO 13451
; LENGTH: 239
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 57-LIB34-060-Q1-E1-G2
US-09-960-352-13451

Query Match 84.8%; Score 17.8; DB 9; Length 239;
Best Local Similarity 90.5%; Pred. No. 63;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCAAGTCAACAGCTAGTTGT 21
Db 111 CCAATCTCAACAGCTAGTTGT 131

RESULT 5
US-09-960-352-2998
; Sequence 2998, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2998
; LENGTH: 242
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 13-LIB34-054-Q1-E1-D1
US-09-960-352-2998

Query Match 84.8%; Score 17.8; DB 9; Length 242;
Best Local Similarity 90.5%; Pred. No. 64;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCAAGTCAACAGCTAGTTGT 21
Db 142 CCAATCTCAACAGCTAGTTGT 162

RESULT 6
US-09-960-352-183
; Sequence 183, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 183
; LENGTH: 247
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 01-LIB34-051-Q1-E1-A9
US-09-960-352-183

Query Match 84.8%; Score 17.8; DB 9; Length 247;
Best Local Similarity 90.5%; Pred. No. 64;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GenCore version 5.1.6
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CM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:14 ; Search time 9.08108 Seconds

(without alignments)
1643.699 Million cell updates/sec

Title: US-10-088-666-21

Perfect score: 21

Sequence: 1 ccaagtcacaacgtactgt 21

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents NA:

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCUTS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16.2	77.1	525	US-09-248-796A-1527	Sequence 1527, Ap
C 2	16.2	77.1	963	US-09-328-352-3811	Sequence 3811, Ap
C 3	16.2	77.1	8878	US-08-759-444-2	Sequence 2, Appl
C 4	16.2	77.1	9880	US-08-680-897-1	Sequence 1, Appl
C 5	15.8	75.2	996	US-09-094-557-33	Sequence 33, Appl
C 6	15.8	75.2	1050	US-09-134-000C-2255	Sequence 2255, Ap
C 7	15.8	75.2	1053	US-09-071-035-409	Sequence 409, Appl
C 8	15.8	75.2	2666	US-09-524-101D-21	Sequence 21, Appl
C 9	15.4	73.3	780	US-09-248-796A-6461	Sequence 6461, Ap
C 10	15.4	73.3	1380	US-09-328-352-537	Sequence 537, Ap
C 11	15.2	72.4	735	US-09-248-796A-6839	Sequence 6839, Ap
C 12	15.2	72.4	1610	US-09-059-769-19	Sequence 19, Appl
C 13	15.2	72.4	2209	US-09-489-847-16	Sequence 16, Appl
C 14	15.2	72.4	3070	US-09-799-451-652	Sequence 652, App
C 15	15.2	72.4	13508	US-08-956-171E-120	Sequence 120, App
C 16	15.2	72.4	13508	US-08-956-171E-120	Sequence 120, App
C 17	14.8	70.5	36	US-08-612-895A-9	Sequence 9, Appl
C 18	14.8	70.5	36	US-09-093-293-9	Sequence 9, Appl
C 19	14.8	70.5	36	US-09-459-553-9	Sequence 9, Appl
C 20	14.8	70.5	36	US-09-882-246-9	Sequence 9, Appl
C 21	14.8	70.5	36	PCT-US94-10562A-9	Sequence 9, Appl
C 22	14.8	70.5	5749	US-09-602-757A-45	Sequence 45, Appl
C 23	14.6	69.5	105	US-09-206-942-9	Sequence 9, Appl
C 24	14.6	69.5	127	US-08-956-171E-4780	Sequence 4780, Ap
C 25	14.6	69.5	127	US-08-781-986A-4780	Sequence 4780, Ap
C 26	14.6	69.5	267	US-09-253-991A-6214	Sequence 6214, Ap
C 27	14.6	69.5	300	US-08-956-171E-4419	Sequence 4419, Ap

28	14.6	69.5	300	US-08-781-986A-4419	Sequence 4419, Ap
29	14.6	69.5	302	US-08-956-171E-4448	Sequence 4448, Ap
30	14.6	69.5	302	US-08-781-986A-4448	Sequence 4448, Ap
C 31	14.6	69.5	355	US-08-956-171E-4233	Sequence 4233, Ap
C 32	14.6	69.5	355	US-08-781-986A-4233	Sequence 4233, Ap
C 33	14.6	69.5	359	US-08-956-171E-4081	Sequence 4081, Ap
C 34	14.6	69.5	359	US-08-781-986A-4081	Sequence 4081, Ap
C 35	14.6	69.5	361	US-08-956-171E-4071	Sequence 4071, Ap
C 36	14.6	69.5	361	US-08-781-986A-4071	Sequence 4071, Ap
C 37	14.6	69.5	400	US-08-956-171E-3652	Sequence 3652, Ap
C 38	14.6	69.5	400	US-08-781-986A-3652	Sequence 3652, Ap
C 39	14.6	69.5	400	US-08-956-171E-3756	Sequence 3756, Ap
C 40	14.6	69.5	400	US-08-781-986A-3756	Sequence 3756, Ap
C 41	14.6	69.5	400	US-08-956-171E-4470	Sequence 4470, Ap
C 42	14.6	69.5	400	US-08-781-986A-3647	Sequence 3647, Ap
C 43	14.6	69.5	400	US-08-956-171E-3652	Sequence 3652, Ap
C 44	14.6	69.5	400	US-08-781-986A-3756	Sequence 3756, Ap
45	14.6	69.5	400	US-08-781-986A-3843	Sequence 3843, Ap

ALIGNMENTS

RESULT 1
US-09-248-796A-1527/c
Sequence 1527, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248, 796A
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074, 725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096, 409
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 1527
LENGTH: 525
TYPE: DNA
ORGANISM: Candida albicans
US-09-248-796A-1527

Query Match 77.1%, Score 16.2, DB 4, Length 525,
Best Local Similarity 85.7%, Pred. No. 62,
Matches 18, Conservative 0, Mismatches 3, Indels 0, Gaps 0,

QY 1 CCAAGTCACAACGTACTGT 21
Db 279 CCAAGTCACAACCTGTTT 259

RESULT 2
US-09-328-352-3811
Sequence 3811, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Berton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328, 352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 3811
LENGTH: 963
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-3811

Query Match 77.1%, Score 16.2, DB 4, Length 963,

Best Local Similarity 85.7%; Pred. No. 69;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCAAGTCACACGAGTGTGT 21
Db 382 CCAAGTCACACGAGTGTAT 402

RESULT 3

US-08-759-444-2/c
Sequence 2, Application US/08759444
Patent No. 5824309
GENERAL INFORMATION:
APPLICANT: Dassarma, Shiladitya
APPLICANT: Moished, Fazeela
APPLICANT: Stuart, Elizabeth
APPLICANT: Black, Samuel
TITLE OF INVENTION: RECOMBINANT GAS VESICLES AND USES THEREOF
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,444
FILING DATE: 05-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/008,200
FILING DATE: 05-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07880/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8878 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-759-444-2

Query Match 77.1%; Score 16.2; DB 1; Length 8878;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCAAGTCACACGAGTGTGT 21
Db 6765 CCAAGTCACACGAGTGTGT 6745

RESULT 4
US-08-680-897-1/c
Sequence 1, Application US/08680897
Patent No. 6008051

GENERAL INFORMATION:
APPLICANT: Dassarma, Shiladitya
APPLICANT: Halladay, John
APPLICANT: Ng, Wai-lap
TITLE OF INVENTION: RECOMBINANT VECTOR AND PROCESS FOR CELL
TITLE OF INVENTION: FLUTATION
NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,897
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/271,270
FILING DATE:
APPLICATION NUMBER: 944,581
FILING DATE: 14-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9880 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-680-897-1

Query Match 77.1%; Score 16.2; DB 3; Length 9880;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCAAGTCACACGAGTGTGT 21
Db 7765 CCAAGTCACACGAGTGTGT 7745

RESULT 5

US-09-094-557-33
Sequence 33, Application US/09094557
Patent No. 6225531
GENERAL INFORMATION:
APPLICANT: Kakitani, Makoto
APPLICANT: Umemoto, Naoyuki
APPLICANT: Ishida, Isao
APPLICANT: Iwamatsu, Akihito
APPLICANT: Yoshikawa, Masaki
APPLICANT: Yamaoka, Naoto
TITLE OF INVENTION: GLUCAN ELICITOR RECEPTOR, DNA MOLECULE
TITLE OF INVENTION: CODING THEREFOR, FUNGUS-RESISTANT PLANTS TRANSFORMED WITH
TITLE OF INVENTION: THE DNA MOLECULE AND METHOD FOR CREATING THE PLANTS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:13 ; Search time 40.7387 Seconds
(without alignments)
2705.971 Million cell updates/sec

Title: US-10-088-666-21

Perfect score: 21

Sequence: 1 ccaagtcacacagctagctgc 21

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003s:*
7: Geneseq2004s:*
8: Geneseq2005s:*
9: Geneseq2006s:*
10: Geneseq2007s:*
11: Geneseq2008s:*
12: Geneseq2009s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	5	AAF61586 Lactobac
2	21	100.0	267	5	AAF61586 Lactobac
3	18	85.7	2215	3	AAZ43884 C. victin
4	17.8	84.8	207	8	ABX39064 Bovine ES
5	17.8	84.8	211	8	ABX36896 Bovine ES
6	17.8	84.8	229	8	ABX39055 Bovine ES
7	17.8	84.8	239	8	ABX48286 Bovine ES
8	17.8	84.8	242	8	ABX37833 Bovine ES
9	17.8	84.8	247	8	ABX35018 Bovine ES
10	17.8	84.8	292	8	ABX42572 Bovine ES
11	17.8	84.8	301	8	ABX34921 Bovine ES
12	17.8	84.8	308	8	ABX45227 Bovine ES
13	17.8	84.8	340	8	ABX37596 Bovine ES
14	17.8	84.8	341	8	ABX37026 Bovine ES
15	17.8	84.8	342	8	ABX46317 Bovine ES
16	17.8	84.8	348	8	ABX44238 Bovine ES
17	17.8	84.8	358	8	ABX43307 Bovine ES
18	17.8	84.8	360	8	ABX35914 Bovine ES
19	17.8	84.8	360	8	ABX47692 Bovine ES
20	17.8	84.8	366	8	ABX43494 Bovine ES
21	17.8	84.8	366	8	ABX48929 Bovine ES

22	17.8	84.8	368	8	ABX39058	ABX39058 Bovine ES
23	17.8	84.8	378	8	ABX37801	ABX37801 Bovine ES
24	17.8	84.8	382	8	ABX35050	ABX35050 Bovine ES
25	17.8	84.8	385	8	ABX45476	ABX45476 Bovine ES
26	17.8	84.8	391	8	ABX45430	ABX45430 Bovine ES
27	17.8	84.8	395	8	ABX37340	ABX37340 Bovine ES
28	17.8	84.8	398	8	ABX41848	ABX41848 Bovine ES
29	17.8	84.8	399	8	ABX44231	ABX44231 Bovine ES
30	17.8	84.8	404	8	ABX35014	ABX35014 Bovine ES
31	17.8	84.8	404	8	ABX37630	ABX37630 Bovine ES
32	17.8	84.8	405	8	ABX42081	ABX42081 Bovine ES
33	17.8	84.8	405	8	ABX47215	ABX47215 Bovine ES
34	17.8	84.8	407	8	ABX44681	ABX44681 Bovine ES
35	17.8	84.8	416	8	ABX46352	ABX46352 Bovine ES
36	17.8	84.8	417	8	ABX44888	ABX44888 Bovine ES
37	17.8	84.8	419	8	ABX42344	ABX42344 Bovine ES
38	17.8	84.8	420	8	ABX40952	ABX40952 Bovine ES
39	17.8	84.8	427	8	ABX42638	ABX42638 Bovine ES
40	17.8	84.8	430	8	ABX40746	ABX40746 Bovine ES
41	17.8	84.8	458	8	ABX33980	ABX33980 Bovine ES
42	17.8	84.8	553	6	ABN73905	ABN73905 Bovine em
43	17.8	84.8	586	6	ABN73190	ABN73190 Bovine em
44	17.8	84.8	606	6	ABN73809	ABN73809 Bovine em
45	17.8	84.8	641	6	ABN73340	ABN73340 Bovine em

ALIGNMENTS

RESULT 1
AAF61586
ID AAF61586 standard; DNA; 21 BP.
XX
AC AAF61586;
XX
DT 02-JUL-2001 (first entry)
XX
DE Lactobacillus brevis 23S rRNA/5S rRNA specific DNA probe.
XX
KW 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.
XX
OS Lactobacillus brevis.
XX
PN DE19945964-A1.
XX
PD 05-APR-2001.
XX
PF 24-SEP-1999; 99DE-01045964.
XX
PR 24-SEP-1999; 99DE-01045964.
XX
PA (BIOT) BIOTECOM DIAGNOSTICS GMBH.
XX
PI Fandke M, Gasch A, Berghof K;
XX
DR WPI; 2001-246136/26.
XX
PT Detecting contaminating microorganisms in brewing, by nucleic acid
PT amplification and hybridization, either non-specific or genus- or species
PT -specific.
XX
PS Claim 9(i); Page 15; 48pp; German.
XX
XX This invention describes a novel method for detecting microorganisms (A)
XX of importance in brewing which comprises treating a sample with at least
XX two primers (P1) that hybridize to a consensus region in the nucleic acid
XX of (A), at least part of the microbial nucleic acid is amplified, the
XX amplicon is treated with at least one probe (P2) that hybridizes
XX specifically with a sequence common to all (A) or specific for one or
XX more families, genera or species, and any formation of hybrids is
XX detected. The method is used to detect, identify and/or characterize
XX microorganisms in beer or brewing materials, particularly for detecting
XX contamination. The method may detect the entire range of contaminating

CC microbes, either as a general test for contamination or as a test
 CC specific for particular genera or (sub)species. It is quicker than known
 CC microbiological methods, and can detect several organisms in the same
 CC sample, including organisms not presently recognized as contaminants. The
 CC method provides an early indication of contamination and can be automated
 CC for high throughput analysis

XX Sequence 21 BP; 7 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 5; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAAGTCACACGCTAGTGT 21
 1 CCAAGTCACACGCTAGTGT 21

Db 1 CCAAGTCACACGCTAGTGT 21

RESULT 2

AA61566

ID AA61566 standard; DNA; 267 BP.

XX AA61566;

DT 02-JUL-2001 (first entry)

DE Lactobacillus brevis 23S rRNA-spacer-5S rRNA DNA fragment.

KM 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.

OS Lactobacillus brevis.

PN DE19945964-A1.

PD 05-APR-2001.

PF 24-SEP-1999; 99DE-01045964.

PR 24-SEP-1999; 99DE-01045964.

PA (BIOT-) BIOTECON DIAGNOSTICS GMBH.

PI Fandke M, Gasch A, Berghof K;

DR WPI; 2001-246136/26.

XX Detecting contaminating microorganisms in brewing, by nucleic acid
 PT amplification and hybridization, either non-specific or genus- or species
 PT -specific.

PS Claim 9(1); Page 9; 48pp; German.

XX This invention describes a novel method for detecting microorganisms (A)
 CC of importance in brewing which comprises treating a sample with at least
 CC two primers (P1) that hybridize to a consensus region in the nucleic acid
 CC of (A), at least part of the microbial nucleic acid is amplified, the
 CC amplicon is treated with at least one probe (P2) that hybridizes
 CC specifically with a sequence common to all (A) or specific for one or
 CC more families, genera or species, and any formation of hybrids is
 CC detected. The method is used to detect, identify and/or characterize
 CC microorganisms in beer or brewing materials, particularly for detecting
 CC contamination. The method may detect the entire range of contaminating
 CC microbes, either as a general test for contamination or as a test
 CC specific for particular genera or (sub)species. It is quicker than known
 CC microbiological methods, and can detect several organisms in the same
 CC sample, including organisms not presently recognized as contaminants. The
 CC method provides an early indication of contamination and can be automated
 CC for high throughput analysis

XX Sequence 267 BP; 77 A; 51 C; 77 G; 62 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 5; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAAGTCACACGCTAGTGT 21

Db 103 CCAAGTCACACGCTAGTGT 123

RESULT 3

AAZ43864/C

ID AAZ43864 standard; cDNA; 2215 BP.

XX AAZ43864;

DT 10-MAR-2000 (first entry)

DE C. vicina LSP-2 cDNA.

KM Arylphorin; calliphorin; ABP; receptor-binding domain; plant protection;

KM hygiene; veterinary medicine; LSP-2; ds.

OS Calliphora vicina.

OS Calliphora vicina.

PN DE19824492-A1.

PD 09-DEC-1999.

PF 02-JUN-1998; 98DE-01024492.

PR 02-JUN-1998; 98DE-01024492.

PA (FARB) BAYER AG.

PI Scheller K, Hansen I, Gutschmann V, Turberg A;

DR WPI; 2000-054341/05.

DR P-PSDB; AAY51007.

XX Receptor-binding domain useful for identifying new substances for plant

PT protection, hygiene or veterinary medicine.

PS Example A; Page 40-43; 50pp; German.

XX This invention describes novel receptor-binding domain of the Calliphora
 CC vicina arylphorin protein (also known as calliphorin). The receptor-
 CC binding domain, nucleic acid constructs, host cells and antibodies
 CC described in the invention are useful for discovering new active
 CC substances for plant protection, hygiene or veterinary medicine, in
 CC particular for combination, which influences the interaction between
 CC arylphorin and the arylphorin receptor. This sequence encodes the C.
 CC vicina LSP-2 protein

XX Sequence 2215 BP; 634 A; 524 C; 433 G; 624 T; 0 U; 0 Other;

Query Match 85.7%; Score 18; DB 3; Length 2215;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAAGTCACACGCTAGT 18
 1687 CCAAGTCACACGCTAGT 1670

Db 1687 CCAAGTCACACGCTAGT 1670

RESULT 4

ABX39064

ID ABX39064 standard; cDNA; 207 BP.

XX ABX39064;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:13 ; Search time 4454.01 Seconds
(without alignments)
2184.416 Million cell updates/sec

Title: US-10-088-666-1

Perfect score: 267

Sequence: 1 tatatggaagcgaagaccctc.....agtagtcggggatcgcgcc 267

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163.4	61.2	793	B2369094	Cot100.1.
2	105.4	39.5	3268	BH770998	LMGtag72
3	105.4	39.5	6499	BH771024	LMGtag74
4	58.2	21.8	342	CR469421	CR469421
5	58.4	21.1	690	BH687637	BH687637
6	51.6	19.3	1258	CR477397	CR477397
7	50.4	18.9	1258	BH770957	BH770957
8	50.2	18.8	391	AO990586	AO990586
9	50.2	18.8	607	AO989492	AO989492
10	49.2	18.4	393	CC144308	CC144308
11	48.2	18.4	453	BH003208	BH003208
12	48.2	18.4	833	CL659016	CL659016
13	48.6	18.2	844	CL664279	CL664279
14	48.6	18.2	872	CL662374	CL662374
15	48.6	18.2	879	CL667131	CL667131
16	47.2	17.7	255	BH770635	BH770635
17	47.2	17.7	333	CR470260	CR470260
18	47.2	17.6	698	AG613316	AG613316
19	46	17.2	534	CL681720	CL681720
20	46	17.2	664	AG613279	AG613279
21	46	17.2	735	CL667389	CL667389
22	45.8	17.2	544	AO989631	AO989631
23	45.8	17.2	655	AO990982	AO990982
24	44.8	16.8	1073	AF114216	AF114216

C 25	44.4	16.6	646	9	CL660916	CL660916
C 26	44.4	16.6	685	9	CL656043	CL656043
C 27	44.4	16.6	786	9	CL654528	CL654528
C 28	44.4	16.6	811	9	CL673498	CL673498
C 29	44.4	16.6	820	9	CL668272	CL668272
C 30	44.2	16.6	643	2	AM948147	AM948147
C 31	44	16.5	381	1	AUI80248	AUI80248
C 32	44	16.5	814	7	CNS86292	CNS86292
C 33	43.8	16.4	1101	8	AF029514	AF029514
C 34	43.6	16.3	351	1	AF1903023	AF1903023
C 35	43.2	16.2	1197	4	BZ579062	BZ579062
C 36	42.6	16.1	343	4	B1895648	B1895648
C 37	42.6	16.0	330	2	BE092318	BE092318
C 38	42.6	16.0	694	2	AM948136	AM948136
C 39	42.6	16.0	730	2	AM948130	AM948130
C 40	42.6	16.0	738	2	AM948138	AM948138
C 41	42.4	15.9	158	2	AM858409	AM858409
C 42	42.4	15.9	282	7	CN025695	CN025695
C 43	42.4	15.9	518	5	BX548956	BX548956
C 44	42.4	15.9	548	5	BX548957	BX548957
C 45	42.4	15.9	791	9	CL670555	CL670555

ALIGNMENTS

RESULT 1
B2369094
LOCUS
DEFINITION
Cot100.1.2.D04 Maize Cot100 library Zea mays genomic, genomic
survey sequence.

ACCESSION
B2369094
VERSION
B2369094.1
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS
Yuan, Y., Sammlinger, P. and Bennetzen, J. L.
TITLE
High Cot sequence analysis of the maize genome
JOURNAL
Unpublished (2003)
COMMENT
Contact: Bennetzen JL
Department of Biological Sciences
Purdue University
Hansen 339#, Purdue University, West Lafayette, IN 47907, USA
Tel: 765 494 4919
Fax: 765 496 1496
Email: maize@dlb.bio.purdue.edu

Forward and reverse reads were assembled when significant overlap was detected.
Seq primer: T7 and T3
Class: shotgun.
Location/Qualifiers
1..793
/organism="Zea mays"
/mol_type="genomic DNA"
/culti_var="B73"
/db_xref="taxon:4577"
/dev_stage="10 days seedling"
/lab_host="D10B"
/clone_lib="Maize Cot100 library"
/note="Organ: young leaves; Vector: pcr4TOPO; Maize genomic DNA was sheared to fragments averaging about 1.8 kb, was denatured and then reassociated in 1 x SSC at 65°C. After a given Cot value was reached, aliquots were run over a hydroxyapatite (HAP) column in order to separate single stranded DNA from double stranded DNA. The single stranded DNA was then converted to a double stranded form with one round of Klenow DNA polymerase treatment with random 9-mer primers. The double-stranded fragments were then further size-selected over an agarose

FEATURES

source

ORIGIN gel and cloned into the PCR4 TOPO vector."

```

Query Match      61.2%; Score 163.4; DB 8; Length 793;
Best Local Similarity 81.1%; Pred. No. 1.3e-40;
Matches 215; Conservative 0; Mismatches 46; Indels 4; Gaps 2;

Oy 3 TATGAAGTAAGACCCCTGAGAGATGATCAGTAGATAGCGTGAAGTAGCAGCCCGG 62
Db 132 TTGGAAGTAAGACCCCAAGAGATGATGATGATGATGATGATGATGATGATGATG 191
Oy 63 AGGGGTGAGACCGACCACTATATGCTGAGAGACTTAAACCAAGTCAACAGTATTTG 122
Db 192 AGGATGAGACCGACCACTATATGCTGAGAGACTTAAACCAAGTCAAGTGTGAGGAT 251
Oy 123 TTTCGAGATATATGATATATATCTATGTTTGGAGAGAAAGTCTCTATAGTGTG 182
Db 252 CTTCATG--TGAAAAGATATTTTATGTTTGAACACAG--CTTCAAGGTGTG 307
Oy 183 GCGATAGCTGAGAGATACCTGTTCCATGCGGACACAGAGTTAGCTTCGACG 242
Db 308 ATGATGCGCTGAAGAGATACCTGTTCCATGCGGACACAGAGTTAGCTTCGACG 367
Oy 243 CCGATAGTATGTTGGGGATGCCCC 267
Db 368 CCAAAAGTATGTTGGGGATGCCCC 392

RESULT 2
BH770998 3268 bp DNA linear GSS 01-MAY-2002
LOCUS LIMGtag721 MG1363 Random Sequence Tag Library Lactococcus lactis
DEFINITION subsp. cremoris genomic, genomic survey sequence.
ACCESSION BH770998
VERSION BH770998.1 GI:20373955
KEYWORDS GSS.
SOURCE Lactococcus lactis subsp. cremoris
ORGANISM Lactococcus lactis subsp. cremoris
          Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
          Lactococcus.
REFERENCE 1 (bases 1 to 3268)
AUTHORS Bolotin, A., Ehrlich, S.D. and Sorokin, A.
TITLE Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL Sci. Aliments (2002) In press
COMMENT Contact: Sorokin A
          Genetique Microbiome
          INRA
          CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
          Tel: 33 1 34 65 25 16
          Fax: 33 1 34 65 25 21
          Email: sorokine@jouy.inra.fr
          best homologue in strain IL1403 is dnaG (93%)
          Class: shotgun
          High quality sequence start: 30
          High quality sequence stop: 3240.
          Location/Qualifiers
            1..3268
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              /mol_type="genomic DNA"
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              /sub_species="cremoris"
              /db_xref="taxon:1359"
              /clone_lib="MG1363 Random Sequence Tag Library"
              /note="Vector: pSGMW2; Site 1: SmaI; Library of
              chromosomal fragments of L.lactis strain MG1363 was
              prepared by partial AluI digestion or by sonication."

ORIGIN
Query Match      39.5%; Score 105.4; DB 8; Length 3268;
Best Local Similarity 67.3%; Pred. No. 4.6e-22;
Matches 185; Conservative 0; Mismatches 76; Indels 14; Gaps 2;

7 GAAGTAAGACCCCTGAGAGATGATCAGTAGATAGCTGGAAGTAGAGAGCCCGTAGGC 66

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Db 361 GAATTAAGACCCAGAGATATCTGTAAGTAGAGTAGAGAGAGTTGCGAGAC 420
Oy 67 GTGAGCGGACCACTATATGCTGAGAGACTTAACCA-----GTCAACAC 115
Db 421 TTGAGCGGACCACTATATGCTGAGAGACTTAACCAAGAGTCAATATAATGTC 480
Oy 116 GTAGTGTTCGAGATATATGATATATCTAGTTTGGAGGAGAGAGTCTCTTAG 175
Db 481 TTATGTTTGAAGTAGAGATATGTTTATTTAGTTTGAATGTTCAAGTAACTTTA 540
Oy 176 TG---TGTGGCGATAGCTGAAGATACCTGTTCCATGCGGACACAGAGTTAG 232
Db 541 TGAATTTGCATCATTCATGCGATGAGATACACTGTTCCATGCGGACACAGAGTTAG 600
Oy 233 CTTCAGACGCGGATAGTATGTTGGGAGTCGCCCC 267
Db 601 TCATCTACGCGGAGATCTTGGGGGTTGCCCC 635

RESULT 3
BH771024 6499 bp DNA linear GSS 01-MAY-2002
LOCUS LIMGtag746 MG1363 Random Sequence Tag Library Lactococcus lactis
DEFINITION subsp. cremoris genomic, genomic survey sequence.
ACCESSION BH771024
VERSION BH771024.1 GI:20373981
KEYWORDS GSS.
SOURCE Lactococcus lactis subsp. cremoris
ORGANISM Lactococcus lactis subsp. cremoris
          Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
          Lactococcus.
REFERENCE 1 (bases 1 to 6499)
AUTHORS Bolotin, A., Ehrlich, S.D. and Sorokin, A.
TITLE Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL Sci. Aliments (2002) In press
COMMENT Contact: Sorokin A
          Genetique Microbiome
          INRA
          CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
          Tel: 33 1 34 65 25 16
          Fax: 33 1 34 65 25 21
          Email: sorokine@jouy.inra.fr
          best homologue in strain IL1403 is ywga (78%)
          Class: shotgun
          High quality sequence start: 30
          High quality sequence stop: 6471.
          Location/Qualifiers
            1..6499
              /organism="Lactococcus lactis subsp. cremoris"
              /mol_type="genomic DNA"
              /strain="MG1363"
              /sub_species="cremoris"
              /db_xref="taxon:1359"
              /clone_lib="MG1363 Random Sequence Tag Library"
              /note="Vector: pSGMW2; Site 1: SmaI; Library of
              chromosomal fragments of L.lactis strain MG1363 was
              prepared by partial AluI digestion or by sonication."

ORIGIN
Query Match      39.5%; Score 105.4; DB 8; Length 6499;
Best Local Similarity 67.3%; Pred. No. 5.3e-22;
Matches 185; Conservative 0; Mismatches 76; Indels 14; Gaps 2;

7 GAAGTAAGACCCCTGAGAGATGATCAGTAGATAGCTGGAAGTAGAGAGCCCGTAGGC 66
Db 5177 GAATTAAGACCCAGAGATATCTGTAAGTAGAGTAGAGAGAGTTGCGAGAC 5236
Oy 67 GTGAGCGGACCACTATATGCTGAGAGACTTAACCA-----GTCAACAC 115
Db 5237 TTGAGCGGACCACTATATGCTGAGAGACTTAACCAAGAGTCAATATAATGTC 5296
Oy 116 GTAGTGTTCGAGATATATGATATATCTAGTTTGGAGGAGAGAGTCTCTTAG 175

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:50:19 ; Search time 461.036 Seconds
(without alignments)
3127.876 Million cell updates/sec

Title: US-10-088-666-1

Perfect score: 267

Sequence: 1 tatataggaagaaagacccct.....agtagtgaggagacgcccc 267

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US05_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US04_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US03_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/US02_PUBCOMB.seq:*
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- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115.8	43.4	31702	US-10-398-221-3	Sequence 3, Appl1
2	115.6	43.3	3510	US-08-961-527-53	Sequence 53, Appl1
3	115.6	43.3	3510	US-10-158-844-53	Sequence 53, Appl1
4	115.6	43.3	3989	US-09-070-927A-359	Sequence 359, Appl1
5	115.6	43.3	5048	US-09-884-465A-2	Sequence 2, Appl1
6	115.6	43.3	8411	US-08-961-527-16	Sequence 16, Appl1
7	115.6	43.3	8411	US-10-158-844-16	Sequence 16, Appl1
8	115.6	43.3	11915	US-08-961-527-96	Sequence 96, Appl1
9	115.6	43.3	11915	US-10-158-844-96	Sequence 96, Appl1
10	114.2	42.8	1389	US-10-398-221-3318	Sequence 3318, Ap
11	114.2	42.8	2631	US-10-398-221-1	Sequence 2, Appl1
12	114.2	42.8	5349	US-10-398-221-3795	Sequence 3795, Ap

13	114.2	42.8	319630	US-10-398-221-7	Sequence 7, Appl1
14	114.2	42.8	684707	US-10-398-221-9	Sequence 9, Appl1
15	114.2	42.8	684707	US-10-398-221-9	Sequence 9, Appl1
16	114.2	42.8	1163020	US-10-398-221-10	Sequence 10, Appl1
17	114.2	42.8	3011208	US-10-398-221-2058	Sequence 2058, Ap
18	114.2	42.8	3011208	US-10-398-221-2058	Sequence 2058, Ap
19	114	42.7	9797	US-09-070-927A-550	Sequence 550, App
20	114	42.7	22960	US-09-070-927A-345	Sequence 345, App
21	113.2	42.4	882	US-10-398-221-3395	Sequence 3395, App
22	113.2	42.4	1907	US-10-398-221-1847	Sequence 1847, App
23	113.2	42.4	4199	US-10-398-221-3890	Sequence 3890, App
24	113.2	42.4	6625	US-10-398-221-2041	Sequence 2041, App
25	111.6	41.8	840	US-08-781-986A-508	Sequence 508, App
26	111.6	41.8	840	US-10-329-624-508	Sequence 508, App
27	109.6	41.0	400	US-08-781-986A-3738	Sequence 3738, App
28	109.6	41.0	400	US-10-329-624-3738	Sequence 3738, App
29	106	39.7	400	US-08-781-986A-3624	Sequence 3624, App
30	106	39.7	400	US-10-329-624-3624	Sequence 3624, App
31	104.4	39.1	386	US-08-781-986A-4064	Sequence 4064, App
32	104.4	39.1	386	US-10-329-624-4064	Sequence 4064, App
33	101.2	37.9	6591	US-08-781-986A-3114	Sequence 3114, App
34	101.2	37.9	6591	US-10-329-624-3114	Sequence 3114, App
35	100.8	37.8	400	US-08-781-986A-3768	Sequence 3768, App
36	100.8	37.8	400	US-10-329-624-3768	Sequence 3768, App
37	100.6	37.7	400	US-08-781-986A-3638	Sequence 3638, App
38	100.6	37.7	400	US-08-781-986A-3748	Sequence 3748, App
39	100.6	37.7	400	US-10-329-624-3748	Sequence 3748, App
40	100.6	37.7	400	US-08-781-986A-3757	Sequence 3757, App
41	100.6	37.7	458	US-10-329-624-3757	Sequence 3757, App
42	100.6	37.7	15249	US-08-781-986A-102	Sequence 102, App
43	100.6	37.7	15249	US-10-329-624-102	Sequence 102, App
44	100.6	37.7	30246	US-08-781-986A-56	Sequence 56, Appl
45	100.6	37.7	30246	US-08-781-986A-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-10-398-221-3/c
Sequence 3, Application US/10398221
Publication No. US20040018514A1
GENERAL INFORMATION:
APPLICANT: KUNST, Frederick
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398, 221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
NUMBER OF SEQ. ID NOS: 4025
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 31702
TYPE: DNA
ORGANISM: Listeria innocua
US-10-398-221-3

Query Match 43.4%; Score 115.8; DB 16; Length 31702;
Best Local Similarity 69.7%; Pred. No. 2.3e-26;
Matches 189; Conservative 0; Mismatches 72; Indels 10; Gaps 2;

QY 6 GGAAGTAAGACCCCTGAGAGATGATCAGGTAGTACGCTGGAAGTACGAGCCGCTGAGG 65
DB 30606 GAAAGTAAGATCCCTGAAAGATATATAGGTAGTATGAGTGGAGTGGAGTGA 30547
QY 66 CGTGGAGCGGACCAAGTACTGATGCTGCTGAGAGCTTAACCAAGTCAACAGTATTGTTT 125
DB 30546 CATGGAGCGGACCAAAATGATGATGAGGAGCTTAACCAAAATGAAACGAGT-TAC 30488

QY 61 TGAGCGGTGAGCGGACCACTACTATTCGTCGAGACTTAAACCAAGTCAACAGTACT 120
DB 3228 CGACACATGATCGGACCTAATATAGCTCGAGACTTATCCAAAGTACTGAGATA 3169
QY 121 TGTTCGAGATTAATGATATATCTAGTTTGAAGGAGAGAG-----TTCTCTTAT 173
DB 3168 TGAAGCGCAACGGTTTCTTTAATTGAATAGATTCAATTTAGTAGGATTAAGTACG 3109
QY 174 AGTGTGTGGCGATGACCTGAAAGATACACTGTTCCATCCGCAACACAAAGTTAAG 233
DB 3108 AGTTAGTGAAGATGACCTGAGATACACTGTTACCTGACGAGACGAAAGTTAAG 3049
QY 234 TTCAGCAGCGCGATGATGATGTTGGGGATCGCCCC 267
DB 3048 CCTAGACCGCGGAAGTATGTTGGGGTTGCCCC 3015

RESULT 2
US-08-961-527-16
; Sequence 16, Application US/08961527
; Patent No. 6420135

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA

ZIP: 20850
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961.527

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PB340P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8512

TELEFAX: (301) 309-8504

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 8411 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-961-527-16
Query Match 43.3%; Score 115.6; DB 4; Length 8411;
Best Local Similarity 66.8%; Pred. No. 1.3e-31;
Matches 183; Conservative 0; Mismatches 84; Indels 7; Gaps 1;

QY 1 TATATGAGATTAAGACCCCTGAGATGATCAGGTAGCTGGAAGTACGACGCCG 60
DB 316 TATATATCATGTAAGCCCTGAGATGATCAGGTAGCTGGAAGTACGACGCCG 375
QY 61 TGAGCGGTGAGCGGACCACTACTATCGGTGAGACTTAACCAAGTCAACAGTACT 120
DB 376 CGACACATGATCGGACCTAATATAGCTCGAGACTTATCCAAAGTACTGAGATA 435
QY 121 TGTTCGAGATTAATGATATATCTAGTTTGAAGGAGAGAG-----TTCTCTTAT 173

DB 436 TGAAGCGAAGCGTTTCTTAATTAATGATATTCATTTTGAAGTATTACTGAG 495
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DB 496 AGTTAGTGAAGATGACCTGAGATACACTGTTACCTGACGAGACGAAAGTTAAG 555
QY 234 TTCAGCAGCGCGATGATGATGTTGGGGATCGCCCC 267
DB 556 CCTAGACCGCGGAAGTATGTTGGGGTTGCCCC 589

RESULT 3
US-08-961-527-96
; Sequence 96, Application US/08961527
; Patent No. 6420135

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA

ZIP: 20850
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961.527

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PB340P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8512

TELEFAX: (301) 309-8504

INFORMATION FOR SEQ ID NO: 96:

SEQUENCE CHARACTERISTICS:

LENGTH: 11915 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-961-527-96
Query Match 43.3%; Score 115.6; DB 4; Length 11915;
Best Local Similarity 66.8%; Pred. No. 1.6e-31;
Matches 183; Conservative 0; Mismatches 84; Indels 7; Gaps 1;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:13 ; Search time 517.964 Seconds
(without alignments)
2705.971 Million cell updates/sec

Title: US-10-088-666-1

Perfect score: 267
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Sequence: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Scoring table: 4134886 seqs, 2624710521 residues

Searched: Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: Geneseqn2000s:*
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5: Geneseqn2001bs:*
6: Geneseqn2002s:*
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8: Geneseqn2003s:*
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10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	156.4	88.6	317	5	AA61572 L. coryni
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4	143.6	53.8	326	5	AA61567 Lactobac
5	139.4	52.2	335	5	AA61574 Pediococ
6	138.2	51.8	326	5	AA61575 Pediococ
7	136.4	51.1	336	5	AA61573 Lactobac
8	131	49.1	110000	10	AD677343_05
9	131	49.1	110000	10	AD677343_07
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12	120	44.9	110000	9	AD612064_05
13	120	44.9	110000	9	AD612064_14
14	119.2	44.6	338	5	AA61570 Lactobac
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41	114.2	42.8	110000	6	ABQ67197_03	Continuation (34 o
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ALIGNMENTS

RESULT 1
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ID AA61566 standard; DNA; 267 BP.
AC AA61566;
DT 02-JUL-2001 (first entry)
XX
XX Lactobacillus brevis 23S rRNA-spacer-5S rRNA DNA fragment.
DE Lactobacillus brevis 23S rRNA-spacer-5S rRNA DNA fragment.
XX
XX 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.
OS Lactobacillus brevis.
XX
XX DE19945964-AL.
XX
XX 05-APR-2001.
XX
XX 24-SEP-1999; 99DE-01045964.
XX
XX 24-SEP-1999; 99DE-01045964.
XX
XX (BIOT-) BIOTECON DIAGNOSTICS GMBH.
XX
XX Pandke M, Gasch A, Berghof K;
XX WPI; 2001-246136/26.
XX
XX Detecting contaminating microorganisms in brewing, by nucleic acid
PT amplification and hybridization, either non-specific or genus- or species
PT -specific.
XX
XX Claim 9(1); Page 9; 48pp; German.
XX
XX This invention describes a novel method for detecting microorganisms (A)
XX of importance in brewing which comprises treating a sample with at least
XX two primers (P1) that hybridize to a consensus region in the nucleic acid
XX of (A), at least part of the microbial nucleic acid is amplified, the
XX amplicon is treated with a sequence common to all (A) or specific for one or
XX more families, genera or species, and any formation of hybrids is
XX detected. The method is used to detect, identify and/or characterize
XX microorganisms in beer or brewing materials, particularly for detecting
XX contamination. The method may detect the entire range of contaminating

microbes, either as a general test for contamination or as a test specific for particular genera or (sub) species. It is quicker than known microbiological methods, and can detect several organisms in the same sample, including organisms not presently recognized as contaminants. The method provides an early indication of contamination and can be automated for high throughput analysis

Sequence 267 BP; 77 A; 51 C; 77 G; 62 T; 0 U; 0 Other;

Query Match 100.0%; Score 267; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 4.5e-63;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 CGCGATAGTAGTTGGGGGATCGCCCC 267
DB 241 CGCGATAGTAGTTGGGGGATCGCCCC 267
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RESULT 2
AAFe1572
ID AAF61572 standard; DNA; 317 BP.

AAFe1572;

02-JUL-2001 (first entry)

L. coryniformis ssp torquens 23S rRNA-spacer-5S rRNA DNA fragment.

23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.

Lactobacillus coryniformis.

DE19945964-A1.

05-APR-2001.

24-SEP-1999; 99DE-01045964.

24-SEP-1999; 99DE-01045964.

(BIOT-) BIOTECON DIAGNOSTICS GMBH.

Fandke M, Gasch A, Berghof K;

WPI; 2001-246136/26.

Detecting contaminating microorganisms in brewing, by nucleic acid amplification and hybridization, either non-specific or genus- or species specific.

Claim 9(i); Page 10; 48pp; German.

This invention describes a novel method for detecting microorganisms (A) of importance in brewing which comprises treating a sample with at least two primers (P1) that hybridize to a consensus region in the nucleic acid of (A), at least part of the microbial nucleic acid is amplified, the amplicon is treated with at least one probe (P2) that hybridizes

specifically with a sequence common to all (A) or specific for one or more families, genera or species, and any formation of hybrids is detected. The method is used to detect, identify and/or characterize microorganisms in beer or brewing materials, particularly for detecting contamination. The method may detect the entire range of contaminating microbes, either as a general test for contamination or as a test specific for particular genera or (sub) species. It is quicker than known microbiological methods, and can detect several organisms in the same sample, including organisms not presently recognized as contaminants. The method provides an early indication of contamination and can be automated for high throughput analysis

Sequence 317 BP; 90 A; 59 C; 96 G; 72 T; 0 U; 0 Other;

Query Match 58.6%; Score 156.4; DB 5; Length 317;
Best Local Similarity 78.3%; Pred. No. 3.1e-44;
Matches 216; Conservative 0; Mismatches 51; Indels 9; Gaps 2;

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DB 24 TTTATGAGTAAGACCCCTGAGAGATCATAGTAATAGCTGAGAGTAAGACGCCCG 83
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DB 232 GCTTCAGACGCGCGATAGTAGTTGGGGATCGCCCC 267
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DB 264 GCTTCAGACGCGCGATAGTAGTTGGGGATCGCCCC 299
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RESULT 3
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ID AAF61571 standard; DNA; 317 BP.

AAFe1571;

02-JUL-2001 (first entry)

L. coryniformis ssp coryniformis 23S rRNA-spacer-5S rRNA DNA fragment.

23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.

Lactobacillus coryniformis.

DE19945964-A1.

05-APR-2001.

24-SEP-1999; 99DE-01045964.

24-SEP-1999; 99DE-01045964.

(BIOT-) BIOTECON DIAGNOSTICS GMBH.

Fandke M, Gasch A, Berghof K;

WPI; 2001-246136/26.

Detecting contaminating microorganisms in brewing, by nucleic acid amplification and hybridization, either non-specific or genus- or species specific.

Claim 9(i); Page 10; 48pp; German.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:13 ; Search time 2085.49 Seconds
(without alignments)
6054.391 Million cell updates/sec

Title: US-10-088-666-1

Perfect score: 267
Sequence: 1 tatatcgaaagtaagacccccc.....agtagtcggggagtcgcccc 267

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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4: gb_om: *
5: gb_ov: *
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7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_pro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	171.8	64.3	298050	AL935261	Lactobaci
6	171.8	64.3	324050	AL935253	Lactobaci
7	156.4	58.6	317	AX105734	Sequence
8	156.4	58.6	317	AX105735	Sequence
9	143.6	53.8	326	AX105730	Sequence
10	139.4	52.2	335	AX105737	Sequence
11	138.2	51.8	326	AX105738	Sequence
12	136.4	51.1	336	AX105736	Sequence
13	131	49.1	177811	AE017206	Lactobaci
14	131	49.1	183043	AE017207	Lactobaci
15	131	49.1	300478	AE017201	Lactobaci
16	131	49.1	300886	AE017205	Lactobaci
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C	31	115.6	43.3	10068	1	AE007489	Streptoco
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO0123605.
ACCESSION AX105729
VERSION AX105729.1 GI:13921742
KEYWORDS
SOURCE Lactobacillus brevis
ORGANISM Lactobacillus brevis
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.

REFERENCE

1. Pandke, M., Gasch, A. and Berghof, K.
Method and nucleic acids for determining the presence of
micro-organisms specific to the brewing process
Patent: WO 0123605-A 1 05-APR-2001;
Biotecon Diagnostics GmbH (DE)
Location/Qualifiers

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Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 ORGANISM Lactobacillus plantarum WCFS1
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 Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 Lactobacillus.

REFERENCE 1
 AUTHORS Kieerebezen, M., Boekhorst, J., van Kranenburg, R., Molenaar, D.,
 Kuisers, O.P., Leer, R., Tarchini, R., Peters, S.A., Sandbrink, H.M.,
 Piers, M.W.E.J., Stiekema, M., Lankhorst, R.V.K., Bron, P.A.,
 Hoffer, S.M., Groot, M.N.N., Kerkhoven, R., de Vries, M., Ursing, B., de
 Vos, W.M. and Stezen, R.J.
 Complete genome sequence of Lactobacillus plantarum WCFS1
 Proc. Natl. Acad. Sci. U.S.A. 100 (4), 1990-1995 (2003)
 JOURNAL 22460236
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 PUBMED 2 (bases 1 to 269050)
 REFERENCE Kieerebezen, M. and Stezen, R.J.
 AUTHORS Direct Submission
 TITLE Submitted (14-OCT-2002) Wageningen Centre for Food Sciences, P.O.
 JOURNAL Box 557, 6700 AN Wageningen, The Netherlands
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 12:43:29 ; Search time 2084.68 Seconds
(without alignments)
6056.719 Million cell updates/sec

Title: US-10-088-666-1

Perfect score: 267

Sequence: 1 tatattggaagaaagaccct.....agtagtcggggagatgcgcc 267

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word-size: 10

Total number of hits satisfying chosen parameters: 1357868

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: listing first 100 summaries

Database :

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1: gb_ba:*
2: gb_hcg:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	267	100.0	267	6	AX105129 Sequence
2	92	34.5	117	1	LBRNRS
3	73	27.3	326	6	AX105730 Sequence
4	50	18.7	338	6	AX105733 Sequence
5	50	18.7	351	6	AX105731 Sequence
6	50	18.7	414	6	AX105732 Sequence
7	50	18.7	1541	1	AR098107 Lactobaci
8	44	16.5	249	6	AR397133 Sequence
9	44	16.5	3989	6	BD193765 Enterococ
10	44	16.5	9797	6	BD193956 Enterococ
11	44	16.5	22960	6	BD193751 Enterococ
12	44	16.5	17645	1	AE016957 Enterococ
13	44	16.5	177911	1	AE017206 Lactobaci
14	44	16.5	183043	6	AX926717 Sequence
15	44	16.5	300478	1	AE017201 Lactobaci
16	44	16.5	300886	1	AE017205 Lactobaci
17	44	16.5	301488	1	AE016950 Enterococ
18	44	16.5	304454	1	AE016956 Enterococ
19	44	16.5	326434	1	AE016947 Enterococ

20	44	16.5	349980	6	AX926712 Sequence
21	44	16.5	349980	6	AX926713 Sequence
22	40	15.0	317	6	AX105734 Sequence
23	40	15.0	317	6	AX105735 Sequence
24	40	15.0	326	6	AX105738 Sequence
25	40	15.0	335	6	AX105737 Sequence
26	40	15.0	2942	6	BD107241 Base sequ
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 C 96 35 13.1 2725 6 AR485426 Sequence
 C 97 35 13.1 2725 6 AR144790 Sequence
 C 98 35 13.1 2869 1 AR270362 Staphyloc
 C 99 35 13.1 2869 6 AR486316 Sequence
 C 100 35 13.1 2869 6 AX145680 Sequence

ALIGNMENTS

RESULT 1
 AX105729 267 bp DNA linear PAT 30-APR-2001

LOCUS AX105729
 DEFINITION Sequence 1 from Patent WO0123605.
 ACCESSION AX105729
 VERSION AX105729.1 GI:13921742

KEYWORDS
 SOURCE Lactobacillus brevis
 ORGANISM Lactobacillus brevis
 Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 Lactobacillus.

REFERENCE
 AUTHORS Fandke, M., Gasch, A. and Berghof, K.
 TITLE Method and nucleic acids for determining the presence of
 JOURNAL micro-organisms specific to the brewing process
 PATENT: WO 0123605-A 1 05-APR-2001;
 Biotechnon Diagnostics GmbH (DE)

FEATURES
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 Matches 267; Conservative 0; Mismatches 0;

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 DB 61 TGAGGCGTGAGCGGACCACTGATGCTGATGAGGAGTTCACCAAGTCAACAGTGT 120
 QY 121 TCTTTCAGATTAATTAATATATATATCTAGTTTGAAGGAGAGTCTCTATAGTGTG 180
 DB 121 TCTTTCAGATTAATTAATATATATCTAGTTTGAAGGAGAGTCTCTATAGTGTG 180
 QY 181 TGGCGATGAGCTGGAAGATACACCTGTTCCATGCCGAACACAGAGTTAGCTTCACA 240
 DB 181 TGGCGATGAGCTGGAAGATACACCTGTTCCATGCCGAACACAGAGTTAGCTTCACA 240
 QY 241 CGCCGATAGTAGTTGGGGGATGCCCC 267
 DB 241 CGCCGATAGTAGTTGGGGGATGCCCC 267

RESULT 2
 LBRNRS 117 bp DNA linear ECT 06-JUN-2003

LOCUS LBRNRS
 DEFINITION Lactobacillus brevis 5S ribosomal RNA.
 ACCESSION X02026
 VERSION X02026.1 GI:43965
 KEYWORDS 5S ribosomal RNA; ribosomal RNA.
 SOURCE Lactobacillus brevis
 ORGANISM Lactobacillus brevis
 Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 Lactobacillus.

REFERENCE
 AUTHORS Woese, C.R., Luehnsen, K.R., Pribula, C.D. and Fox, G.E.
 TITLE Sequence characterization of 5S ribosomal RNA from eight gram
 JOURNAL positive procarotes
 MEDLINE J. Mol. Evol. 8 (2), 143-153 (1976)
 PUBMED 77009046
 FEATUERS
 source 823342
 Location/Qualifiers

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 DB 1 TGTGTGGGATGAGCTGAGAGTACACCTGTTCCATGCCGAACACAGAGTTAGCTT 60

QY 236 CAGCAGCCGATGATGATGTTGGGATCGCCCC 267
 DB 61 CAGCAGCCGATGATGATGTTGGGATCGCCCC 92

RESULT 3
 AX105730 326 bp DNA linear PAT 30-APR-2001
 LOCUS AX105730
 DEFINITION Sequence 2 from Patent WO0123605.
 ACCESSION AX105730
 VERSION AX105730.1 GI:13921743

KEYWORDS
 SOURCE Lactobacillus lindneri
 ORGANISM Lactobacillus lindneri
 Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 Lactobacillus.

REFERENCE

AUTHORS Fandke, M., Gasch, A. and Berghof, K.
 TITLE Method and nucleic acids for determining the presence of
 JOURNAL micro-organisms specific to the brewing process
 PATENT: WO 0123605-A 2 05-APR-2001;
 Biotechnon Diagnostics GmbH (DE)

FEATURES
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ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 3.5e-30;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 204 ATAGTGTGGTGGGATGAGCTGAGAGTACACCTGTTCCATGCCGAACACAGAGTTAA 263
 QY 232 GCTTCAGACGCC 244
 DB 264 GCTTCAGACGCC 276

RESULT 4
 AX105733 338 bp DNA linear PAT 30-APR-2001
 LOCUS AX105733
 DEFINITION Sequence 5 from Patent WO0123605.
 ACCESSION AX105733
 VERSION AX105733.1 GI:13921746
 KEYWORDS